

Query Match 99.8%; Score 1760; DB 1; Length 255;
Best Local Similarity 99.6%; Pred. No. 1.55e-143;
Matches 238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 17 ESQDPKPEDELHSSKKTGMLNKKVLYDNNHSAIIVKSIDOFLYDLYISIKDTKLG 76
|||
QY 1 ESQDPKPEDELHSSKKTGMLNKKVLYDNNHSAIIVKSIDOFLYDLYISIKDTKLG 60
|||

Db 77 YDNVRFKKNDLADKKDKYVDFGANYIYOCFESKKTNDINSHQDRTCTMGVTE 136
|||
QY 61 YDNVRFKKNDLADKKDKYVDFGANYIYOCFESKKTNDINSHQDRTCTMGVTE 120
|||

Db 137 HNGNQLDKRSITRVFEDGKNLSPDVQTNKKKVTAAQELDYLRHLYLVNKKLYEENNS 196
|||
QY 121 HNGNQLDKRSITRVFEDGKNLSPDVQTNKKKVTAAQELDYLRHLYLVNKKLYEENNS 180
|||

Db 197 PYETGYIKFIENENSFYDMMAPAGDKFDQSKYLMYNDNKMVDSKDVKIEVYLTTRKK 255
|||
QY 181 PYETGYIKFIENENSFYDMMAPAGDKFDQSKYLMYNDNKMVDSKDVKIEVYLTTRKK 239
|||

RESULT 2
ID US-08-580-806-2 STANDARD; PRT; 255 AA.

AC xxxxxx
XX
DT
DE Sequence 2, Application US/08580806
CC Sequence 2, Application US/08580806
CC Patent No. 5935568
CC GENERAL INFORMATION:
CC APPLICANT: Dow, Steve W.
CC APPLICANT: Elmslie, Robyn E.
CC APPLICANT: Potter, Terence A.
CC TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sheridan Ross & McIntosh
CC STREET: 1700 Lincoln Street, Suite 3500
CC CITY: Denver
CC STATE: Colorado
CC COUNTRY: U.S.A.
CC ZIP: 80203
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,806
CC FILING DATE:
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Connell, Gary J.
CC REGISTRATION NUMBER: 32,020
CC REFERENCE/DOCKET NUMBER: 2879-29-C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (303) 863-9700
CC TELEFAX: (303) 863-0223
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 255 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 255 AA; 30159 MM; 364503 CN;

Query Match 99.8%; Score 1760; DB 2; Length 255;
Best Local Similarity 99.6%; Pred. No. 1.55e-143;
Matches 238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 17 ESQDPKPEDELHSSKKTGMLNKKVLYDNNHSAIIVKSIDOFLYDLYISIKDTKLG 76
|||
QY 1 ESQDPKPEDELHSSKKTGMLNKKVLYDNNHSAIIVKSIDOFLYDLYISIKDTKLG 60
|||

Db 77 YDNVRFKKNDLADKKDKYVDFGANYIYOCFESKKTNDINSHQDRTCTMGVTE 136
|||
QY 61 YDNVRFKKNDLADKKDKYVDFGANYIYOCFESKKTNDINSHQDRTCTMGVTE 120
|||

Db 137 HNGNQLDKRSITRVFEDGKNLSPDVQTNKKKVTAAQELDYLRHLYLVNKKLYEENNS 196
|||
QY 121 HNGNQLDKRSITRVFEDGKNLSPDVQTNKKKVTAAQELDYLRHLYLVNKKLYEENNS 180
|||

Db 197 PYETGYIKFIENENSFYDMMAPAGDKFDQSKYLMYNDNKMVDSKDVKIEVYLTTRKK 255
|||
QY 181 PYETGYIKFIENENSFYDMMAPAGDKFDQSKYLMYNDNKMVDSKDVKIEVYLTTRKK 239
|||

RESULT 3
ID US-08-446-918A-4 STANDARD; PRT; 233 AA.

AC xxxxxx
XX
DT
DE Sequence 4, Application US/08446918A
CC Sequence 4, Application US/08446918A
CC Patent No. 5705151
CC GENERAL INFORMATION:
CC APPLICANT: Dow, Steve W.
CC APPLICANT: Elmslie, Robyn E.
CC TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sheridan Ross & McIntosh
CC STREET: 1700 Lincoln Street, Suite 3500
CC CITY: Denver
CC STATE: Colorado
CC COUNTRY: U.S.A.
CC ZIP: 80203
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/446,918A
CC FILING DATE: 18-MAY-1995
CC CLASSIFICATION: 552
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kovarik, Joseph E.
CC REGISTRATION NUMBER: 33,005
CC REFERENCE/DOCKET NUMBER: 2879-29
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (303) 863-9700
CC TELEFAX: (303) 863-0223
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 233 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 233 AA; 27137 MM; 292215 CN;

Query Match 21.3%; Score 375; DB 1; Length 233;
Best Local Similarity 35.0%; Pred. No. 9.01e-22;
Matches 82; Conservative 56; Mismatches 77; Indels 19; Gaps 12;

Db 11 DLKKSSEGTALGNLKIYYNNEKAKENKESHDQFLQHTILKGFTHSWYNDLYD 70
|||
QY 10 ELHRSKSKFTGL-MENK-VLYDDNHVSAIIVKSIDOFLYDLYISIKDTKLGNDNRAVE 67
|||

Db 71 FDSKDIYDKYGRKVDLYGAYGYOC---AGG--T--PNK-TACMGVTLHDNNRLT 120
|||

QY 68 FKNRDLADKXKDYDEGANYQCYSFKTKINDINSNETDCKRKTOMGVTENHNGQLD 127
121 EKKVPIPLMLDGNQNTVPLETVTKTNKNKYVOELDLQARKYLQEKYLYNSDVFDEKVO 180
128 KYRSITVAFVDEGK-NLSPD-VQTNKKKYTAQOELDYLTRHYLVKNKKLYEFN--NSPYE 183
DB 181 RGLIVFHTSTEPSVNYDLFGAQQO-YSNT-LIRIYRDNKKTJNSENMHIDIYLT 232
184 TGYIKF-IENENSFYDMMAPAGDKFDQSKYLMYNDNKKMYDSKDYKLEVLT 236
QY 184 TGYIKF-IENENSFYDMMAPAGDKFDQSKYLMYNDNKKMYDSKDYKLEVLT 236
RESULT 4
ID US-08-580-806-4 STANDARD; PRT; 233 AA.
XX xxxxxx
DE Sequence 4, Application US/08580806
XX
CC Sequence 4, Application US/08580806
CC Patent No. 5935568
CC GENERAL INFORMATION:
CC APPLICANT: Dow, Steve W.
CC APPLICANT: Elmslie, Robyn E.
CC APPLICANT: Porter, Terence A.
CC TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Sheridan Ross & McIntosh
CC STREET: 1700 Lincoln Street, Suite 3500
CC CITY: Denver
CC STATE: Colorado
CC COUNTRY: U.S.A.
CC ZIP: 80203
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,806
CC FILING DATE:
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Connell, Gary J.
CC REGISTRATION NUMBER: 32,020
CC REFERENCE/DOCKET NUMBER: 2879-29-C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (303) 863-9700
CC TELEFAX: (303) 863-0223
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 233 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 233 AA; 27137 MW; 292215 CN;
SQ
Query Match 21.3%; Score 375; DB 2; Length 233;
Best Local Similarity 35.0%; Pred. No. 9.01e-22;
Matches 82; Conservative 56; Mismatches 77; Indels 19; Gaps 12;
DB 11 DLRRKSELOGTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFTDHSWYNDLVD 70
10 ELHSSKFTGL-MENMK-VLDDNHVSAINXSIDQFLYPLILISIKTKLGNANDNVAVE 67
DB 71 FDSQDIYDKYKGVKVDLYGAYGYQC---AGC--T--PKM-TACMTGVTGLDNNRLT 120
68 FKNRDLADKXKDYDEGANYQCYSFKTKINDINSNETDCKRKTOMGVTENHNGQLD 127
DB 121 EKKVPIPLMLDGNQNTVPLETVTKTNKNKYVOELDLQARKYLQEKYLYNSDVFDEKVO 180

QY 128 KYRSITVAFVDEGK-NLSPD-VQTNKKKYTAQOELDYLTRHYLVKNKKLYEFN--NSPYE 183
DB 181 RGLIVFHTSTEPSVNYDLFGAQQO-YSNT-LIRIYRDNKKTJNSENMHIDIYLT 232
184 TGYIKF-IENENSFYDMMAPAGDKFDQSKYLMYNDNKKMYDSKDYKLEVLT 236
QY 184 TGYIKF-IENENSFYDMMAPAGDKFDQSKYLMYNDNKKMYDSKDYKLEVLT 236
RESULT 5
ID US-08-876-781-9 STANDARD; PRT; 27 AA.
XX xxxxxx
DE Sequence 9, Application US/08876781
XX
CC Sequence 9, Application US/08876781
CC Patent No. 5872233
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5872233th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 kb storage
CC COMPUTER: ASP Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/876,781
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: 7676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: Internal fragment
CC ORIGINAL SOURCE: Staphylococcus aureus
CC ORGANISM: Staphylococcus aureus
CC STRAIN: S6
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin B amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 39 to 65
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Jones, C.L.

CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5872233
CC TITLE: Gene from *Staphylococcus aureus*
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
SQ SEQUENCE 27 AA; 3270 MW; 3891 CN;

Query Match 11.4%; Score 201; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.93e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 KSIDQFLYFDLIYSIKPTKLGNDVNR 27
QY 39 KSIDQFLYFDLIYSIKPTKLGNDVNR 65

RESULT 6
ID US-08-165-038-9 STANDARD: PRT: 27 AA.
AC xxxxxx
DT
XX
XX
Sequence 9, Application US/08165038
XX
CC Sequence 9, Application US/08165038
CC Patent No. 5639869
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC TITLE OF INVENTION: Mitogen
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5639869th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
CC COMPUTER: AST Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,038
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORIGINAL SOURCE:

CC ORGANISM: *Staphylococcus aureus*
CC STRAIN: S6
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin B amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 39 to 65
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Jones, C.L.
CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5639869
CC TITLE: Gene from *Staphylococcus aureus*
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
SQ SEQUENCE 27 AA; 3270 MW; 3891 CN;

Query Match 11.4%; Score 201; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.93e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 KSIDQFLYFDLIYSIKPTKLGNDVNR 27
QY 39 KSIDQFLYFDLIYSIKPTKLGNDVNR 65

RESULT 7
ID US-08-876-781-10 STANDARD: PRT: 27 AA.
AC xxxxxx
DT
XX
XX
Sequence 10, Application US/08876781
XX
CC Sequence 10, Application US/08876781
CC Patent No. 5872233
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC TITLE OF INVENTION: Mitogen
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5872233th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
CC COMPUTER: AST Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/876,781
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788

CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORIGINAL SOURCE:
CC ORGANISM: Staphylococcus aureus
CC STRAIN: 56
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin B amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 56 to 82
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Jones, C.L.
CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5872233
CC TITLE: Gene from Staphylococcus aureus
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
CC SEQUENCE 27 AA; 3265 MW; 4119 CN;
SQ
Query Match 11.1%; Score 196; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 4,81e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TKLGNDVNVREFFKNKDLADKRYKRYV 27
QY 56 TKLGNDVNVREFFKNKDLADKRYKRYV 82
RESULT 8
ID US-08-165-038-10 STANDARD; PRT; 27 AA.
XX xxxxxx
AC
XX
DT
XX
Sequence 10, Application US/08165038
DE
XX
CC Sequence 10, Application US/08165038
CC Patent No. 5639869
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC TITLE OF INVENTION: Mitogen
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Thorpe, No. 5639869th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
CC COMPUTER: ASR Advantage NB-SX20

CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,038
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEFAX: (801)566-6633
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORIGINAL SOURCE:
CC ORGANISM: Staphylococcus aureus
CC STRAIN: 56
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin B amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 56 to 82
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Jones, C.L.
CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5639869
CC TITLE: Gene from Staphylococcus aureus
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
CC SEQUENCE 27 AA; 3265 MW; 4119 CN;
SQ
Query Match 11.1%; Score 196; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4,81e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TKLGNDVNVREFFKNKDLADKRYKRYV 27
QY 56 TKLGNDVNVREFFKNKDLADKRYKRYV 82
RESULT 9
ID US-08-165-038-11 STANDARD; PRT; 27 AA.
XX xxxxxx
AC
XX
DT
XX
Sequence 11, Application US/08165038
DE
XX
CC Sequence 11, Application US/08165038
CC Patent No. 5639869
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell

CC TITLE OF INVENTION: Mitogen
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5639869th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 kb storage
CC COMPUTER: AST Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,038
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORGANISM: Staphylococcus aureus
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin C1 amino acid
CC NAME/KEY: sequence having similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 30 to 56
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Bohach, G.A.
CC AUTHORS: Schlievert, P.M.
CC TITLE: Nucleotide sequence of the staphylococcal
CC TITLE: enterotoxin C1 gene and relatedness to
CC TITLE: other pyrogenic exotoxins
CC JOURNAL: Mol. Gen. Genet.
CC VOLUME: 209
CC PAGES: 15-20
CC DATE: 1987
SQ SEQUENCE 27 AA; 3107 MW; 4022 CN;

Db 1 DHVSAATKRSVDFLAHLIYINISD 26
1: ||| :|||:| | ||||:| |
Query Match 6.2%; Score 110; DB 1; Length 27;
Best Local Similarity 61.5%; Pred. No. 1.52e+00;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 30 DNHVSATNKSIDQFLYFDLITSIKD 55

RESULT 10
ID US-08-876-781-11 STANDARD; PRT; 27 AA.
XX xxxxxx
AC
XX
DT
XX

DE Sequence 11, Application US/08876781
XX
CC Sequence 11, Application US/08876781
CC Patent No. 5872233
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC TITLE OF INVENTION: Mitogen
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5872233th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 kb storage
CC COMPUTER: AST Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/876,781
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORGANISM: Staphylococcus aureus
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin C1 amino acid
CC NAME/KEY: sequence having similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 30 to 56
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Bohach, G.A.
CC AUTHORS: Schlievert, P.M.
CC TITLE: Nucleotide sequence of the staphylococcal
CC TITLE: enterotoxin C1 gene and relatedness to
CC TITLE: other pyrogenic exotoxins
CC JOURNAL: Mol. Gen. Genet.
CC VOLUME: 209
CC PAGES: 15-20
CC DATE: 1987
SQ SEQUENCE 27 AA; 3107 MW; 4022 CN;

Db 1 DHVSAATKRSVDFLAHLIYINISD 26
1: ||| :|||:| | ||||:| |
Query Match 6.2%; Score 110; DB 2; Length 27;
Best Local Similarity 61.5%; Pred. No. 1.52e+00;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY	30	DNHVSAINVKSIDQELKEDLDIYSIKD	55
RESULT	11	STANDARD:	PRT; 305 AA.
ID	US-08-946-528-1		
XX	xxxxxx		
AC			
XX			
DT			
XX			
DE	Sequence 1, Application US/08946528		
XX			
CC	Sequence 1, Application US/08946528		
CC	Patent No. 5938746		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Hillman, Jennifer L.		
CC	APPLICANT: Bandman, Olga		
CC	APPLICANT: Lal, Preeti		
CC	APPLICANT: Corley, Neil C.		
CC	TITLE OF INVENTION: ELECTRON TRANSPORT PROTEINS		
CC	NUMBER OF SEQUENCES: 9		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Incyte Pharmaceuticals, Inc.		
CC	STREET: 3174 Porter Dr.		
CC	CITY: Palo Alto		
CC	STATE: CA		
CC	COUNTRY: USA		
CC	ZIP: 94304		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Diskette		
CC	COMPUTER: IBM compatible		
CC	OPERATING SYSTEM: DOS		
CC	SOFTWARE: FASTSEQ for Windows Version 2.0		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/946,528		
CC	FILING DATE: Filed Herewith		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER:		
CC	FILING DATE:		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Billings, Lucy J.		
CC	REGISTRATION NUMBER: 36,749		
CC	REFERENCE/DOCKET NUMBER: PF-0406 US		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 650-855-0555		
CC	TELEFAX: 650-845-4166		
CC	TELEX:		
CC	INFORMATION FOR SEQ. ID NO.: 1:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 305 amino acids		
CC	TYPE: amino acid		
CC	STRANDEDNESS: single		
CC	TOPOLOGY: linear		
CC	IMMEDIATE SOURCE:		
CC	LIBRARY: PROSNOT16		
CC	CLONE: 1709102		
SQ	SEQUENCE 305 AA; 34095 MW; 500339 CN;		
	Query Match 6.2%; Score 109; DB 2; Length 305;		
	Best Local Similarity 28.9%; Pred. No. 1.7e+00;		
	Matches 24; Conservative 25; Mismatches 29; Indels 5; Gaps 5		
Db	192 LQLIRAI-LKVPEPTQCFLFNQTEKDILRDELQAARYPNRKLTFTLDPHPKW	250	
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Oy	126 LDKRSIVRVFEQGN-LTSFDVTGKKKVTAGLEDLYLRHLYLKXKKLLYEENSYET	184	
	: I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Db	251 AYSKGFTADM-IR-EHLPAFGD	271	
	: I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Oy	185 GYIK-FIENENSFWMDMPAPGD	206	
RESULT	12	STANDARD:	PRT; 174 AA.
ID	US-08-261-825-2		

[illegible]

```
CC APPLICANT: The Regents of the University of California
CC TITLE OF INVENTION: CLONED Borrella burgdorferi VIRULENCE
CC TITLE OF INVENTION: PROTEIN
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC City: La Jolla
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/07748A
CC FILING DATE: 16-JUN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: HALL, Ph.D., LISA A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07419/013M01 (P03516)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 678-5070
CC FAX: (619) 678-5099
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 174 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 174 AA; 20290 MW; 153533 CN;
SQ
Query Match      5.6%; Score 99; DB 3; Length 174;
Best local Similarity 29.2%; Pred. No. 8,83e+00;
Matches 26; Conservative 25; Mismatches 32; Indels 6; Gaps 6
Db   65 AKAPEIRGSLRKIGIKEN-SVLADALDVGFIRKSTTDFLSFTIMINSINKYPSIF 123
    :::::|::|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy   6 PKPELHKSSKFETGLMEMRKLVD-NHVSAINVKSIDFL-YDDL-IYS-IKDTKGYNY 61
Db   124 DYLLQLDSDKIDYAERKGKERARENFESY 152
    |::::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy   62 DN-VRVFEKNKDLDKKYKYDVEFGANY 89
RESULT 14
ID US-08-719-124-2 STANDARD; PRT; 174 AA.
XX AC xxxxxx
DX
DY
DE Sequence 2, Application US/08719124
CX Patent No. 5854395
CC GENERAL INFORMATION:
CC APPLICANT: Champion, Cheryl I.
CC APPLICANT: Lovett, Michael A.
CC APPLICANT: Haake, David A.
CC APPLICANT: Miller, James N.
CC APPLICANT: Blanco, David R.
CC TITLE OF INVENTION: CLONED Borrella burgdorferi VIRULENCE
CC TITLE OF INVENTION: PROTEIN
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East, Suite 500
CC CITY: Los Angeles
CC STATE: California
```

```
CC CC COUNTRY : USA
CC CC ZIP : 90067
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER : IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/08/719,124
CC CC FILING DATE: 24-SEP-1996
CC CC CLASSIFICATION: 530
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: 08/261,825
CC CC FILING DATE: 17-JUN-1994
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: TUMARKIN, LISA A.
CC CC REGISTRATION NUMBER: P-38,347
CC CC REFERENCE/DOCKET NUMBER: PD3516
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: (619) 455-5100
CC CC TELEFAX: (619) 455-5110
CC CC INFORMATION FOR SEQ ID NO: 2:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 174 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
SQ SQ SEQUENCE 174 AA; 20290 MM; 153533 CN;

Query Match 5.6%; Score 99; DB 2; Length 174;
Best Local Similarity 29.2%; Pred. No. 8,83e+00;
Matches 26; Conservative 25; Mismatches 32; Indels 6; Gaps 6

Db 65 AKAEIRGSLRKRIKEN-SYLDALDVGCFIKSRITFDLSFLIMNINSLINGYPNSIF 123
Qy 6 PKPDELHKSSFTGLMEMRKYLYDD-NHVSAINVKSIDQFL-YFDL-IYS-IKOTKLGN 61
Db 124 DYLIQLDSDKTDYAERKYGERRAREPFESY 152
Qy 62 DN-VRVFEKNKLADKKYKDYVDVGANY 89

RESULT 15
ID US-08-220-378-3 STANDARD; PRT; 25 AA.
XX AC xxxxxx
XX DT
XX DE Sequence 3, Application US/08220378
XX XX
XX XX
Sequence 3, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
CC CC APPLICANT: Johnson, Howard M.
CC CC APPLICANT: Pontzer, Carol H.
CC CC APPLICANT: Griggs, Nathan D.
CC CC TITLE OF INVENTION: Superantigen Agonist and Antagonist
CC CC TITLE OF INVENTION: Peptides
CC CC NUMBER OF SEQUENCES: 10
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: Saliwanchik & Saliwanchik
CC CC STREET: 2421 N.W. 41st Street, Suite A-1
CC CC City: Gainesville
CC CC STATE: FL
CC CC COUNTRY: USA
CC CC ZIP: 32606
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER : IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CC CURRENT APPLICATION DATA:
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(TM)

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Tabular output not generated.

Sequence:

Scoring table:

Searched: 188963 seqs, 236

Listing first 45

1:geneseqp

Statistics: Mean 32.417; Variance 153.333; scale 0.211

and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1763	100.0	239	1	W66647	Synthetic SEB protein	5.29e-14
2	1760	99.8	255	1	W06737	Staphylococcus enterot	9.88e-14
3	1725	97.8	239	1	R13206	Staphylococcal enterot	1.44e-14
4	1725	97.8	239	1	R15014	Staphylococcal enterot	1.44e-14
5	1176	66.7	239	1	R45015	Staphylococcal enterot	3.93e-92
6	1176	66.7	239	1	R13207	Staphylococcal enterot	3.93e-92
7	1135	64.4	238	1	R45016	Staphylococcal enterot	1.86e-88
8	1107	62.8	238	1	R13208	Staphylococcal enterot	5.97e-86
9	760	43.1	190	1	R11989	Staphylococcus enterot	4.85e-55
10	758	43.0	190	1	R42007	Staphylococcus enterot	7.29e-55
11	756	42.9	190	1	R42012	Staphylococcus enterot	1.09e-54
12	756	42.9	190	1	R41993	Staphylococcus enterot	1.09e-54
13	756	42.9	190	1	R41996	Staphylococcus enterot	1.09e-54
14	755	42.8	190	1	R41992	Staphylococcus enterot	1.34e-54
15	753	42.7	190	1	R42000	Staphylococcus enterot	2.02e-54
16	753	42.7	190	1	R41995	Staphylococcus enterot	2.02e-54
17	752	42.6	190	1	R41994	Staphylococcus enterot	2.47e-54
18	751	42.6	190	1	R41991	Staphylococcus enterot	3.03e-54
19	749	42.5	221	1	R45017	Staphylococcal enterot	4.56e-54
20	749	42.5	221	1	R13209	Staphylococcal pyrogeni	4.56e-54
21	747	42.4	190	1	R42009	Staphylococcus enterot	6.85e-54
22	747	42.4	190	1	R42008	Staphylococcus enterot	6.85e-54
23	746	42.3	190	1	R42008	Staphylococcus enterot	8.39e-54

45	726	41.2	190	R42011	Staphylococcus enterot	8.39e-52
44	728	41.3	251	W59781	Staphylococcus enterot	1.03e-53
43	44	41.4	251	M12148	Staphylococcus enterot	1.03e-53
42	730	41.5	251	M12146	Staphylococcus enterot	1.03e-53
41	732	41.5	190	M12145	Staphylococcus enterot	1.03e-53
40	737	41.8	251	M12147	Staphylococcus enterot	1.03e-53
39	738	41.9	251	M12154	Staphylococcus enterot	1.03e-53
38	738	41.9	251	M12154	Staphylococcus enterot	1.03e-53
37	739	41.9	251	M59798	Staphylococcus enterot	1.03e-53
36	739	41.9	190	R42001	Staphylococcus enterot	1.03e-53
35	740	42.0	251	M12150	Staphylococcus enterot	1.03e-53
34	740	42.0	251	M12150	Staphylococcus enterot	1.03e-53
33	740	42.0	251	M12150	Staphylococcus enterot	1.03e-53
32	740	42.0	190	R42010	Staphylococcus enterot	1.03e-53
31	742	42.1	190	R42006	Staphylococcus enterot	1.03e-53
30	742	42.1	190	R42006	Staphylococcus enterot	1.03e-53
29	742	42.1	190	R42006	Staphylococcus enterot	1.03e-53
28	745	42.3	190	R42003	Staphylococcus enterot	1.03e-53
27	745	42.3	190	R42003	Staphylococcus enterot	1.03e-53
26	745	42.3	190	R42003	Staphylococcus enterot	1.03e-53
25	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
24	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
23	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
22	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
21	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
20	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
19	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
18	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
17	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
16	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
15	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
14	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
13	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
12	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
11	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
10	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
9	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
8	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
7	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
6	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
5	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
4	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
3	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
2	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53
1	746	42.3	190	R42005	Staphylococcus enterot	1.03e-53

ALIGNMENTS

RESULT 1
 ID W64647 standard; peptide: 239 AA.
 AC W64647;
 DT 23-OCT-1998 (first entry)
 DE Synthetic SSB protein fragment.
 KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
 KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
 KW therapeutic; vaccine; food poisoning.
 OS Synthetic.
 OS Staphylococcus aureus.
 PN W09JUL9444-A1.
 PD 09-JUL-1998.
 PF 30-DEC-1997; IL0438.
 PR 30-DEC-1996; IL-119938.
 PA (YISS) YISSUM RES & DEV CO.
 PI Arad G, Kaempfer R;
 DR MPI, 98-388042/33.
 PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
 PT antagonising toxin-mediated activation of T cells and prevention or
 PT treatment of toxic shock caused by exotoxin(s)
 PS Example 8; Page 41; 68pp; English.
 CC W64636-W64657 are peptides homologous to the amino acid sequence of a
 CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
 CC capable of eliciting protective immunity against toxic shock induced
 CC by PET or by a mixture of PETs. Such peptides are also capable of
 CC antagonising toxin-mediated activation of T-cells, inhibiting expression
 CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, INF-gamma or
 CC TNF-beta genes. The peptides may be used to prepare therapeutics or
 CC vaccines for the treatment of prophylaxis of toxin-mediated activation
 CC of T cells and eliciting protective immunity against toxic shock induced
 CC by PETs. They can also be used for the treatment of harmful effects
 CC (especially food poisoning) and toxic shock caused by PET. Antiserum to
 CC the peptides can also be used for alleviating toxic shock induced by PET
 CC sequence 239 AA.

Query Match 100.0%; Score 1763; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 5,29e-145;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Query Match	100.08%	Score 1763	DB 1	length 239
	Best Local Similarity	100.08%	Pred. No. 5,298-145		
	Matches	239	Conservative	0	Mismatches 0; Indels 0; Gaps
Db	1	ESQPDPRDPLDHSKSRKTGMLGNMKVLYDDNNHSAIIVKSIIDQFLYRDLVYSIKPTLGN	60		
QY	1	ESQPDPRDPLDHSKSRKTGMLGNMKVLYDDNNHSAIIVKSIIDQFLYRDLVYSIKPTLGN	60		
Db	61	YDNRVVEFKRKDLADKYDKRYDVFEGANYIYQCYFSKRTINDINSHETDKRKTGMGGVTE	120		
QY	61	YDNRVVEFKRKDLADKYDKRYDVFEGANYIYQCYFSKRTINDINSHETDKRKTGMGGVTE	120		

DB 121 HNGNQLDKRSTIVRFEDEGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 |||
 OY 121 HNGNQLDKRSTIVRFEDEGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 DB 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLAMYNDNKWVDSKDVKIEVYLTTRKK 239
 |||
 OY 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLAMYNDNKWVDSKDVKIEVYLTTRKK 239

RESULT 2

ID M06737 standard; Protein: 255 AA.
 AC M06737;
 DT 08-MAR-1997 (first entry)
 DE Staphylococcus enterotoxin B.
 KM Enterotoxin B: superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
 OS vaccine; adjuvant.
 OS Staphylococcus sp.
 FH Key Location/Qualifiers
 FT peptide 1..15
 FT /label= Sig-peptide
 PN M09636366-A1.
 PD 21-NOV-1996.
 PF 20-MAY-1996; U07432.
 PR 18-MAY-1995; US-446918.
 PR 29-DEC-1995; US-580806.
 PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.
 PI Dow SW, Elmstie RE, Potter RA;
 DR N-PSDB; T45697.
 DR WPI: 97-011857/01.
 PT Recombinant molecule encoding super:antigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer
 PS Example 1: Page 96-97; 131pp; English.
 CC A cDNA clone (T45698) codes for staphylococcal enterotoxin B
 CC (M06737) superantigen. Nucleic acids encoding superantigens (see
 CC also M06738-39), esp. truncated forms of the superantigen lacking
 CC the leader peptide, can be utilised in the gene therapy of cancer,
 CC infectious diseases and immunological disorders. The nucleic acid,
 CC optionally in combination with cytokine or chemokine nucleic acids,
 CC is delivered to an animal using e.g. liposomes. It acts by
 CC controlling the activity of effector cells, such as T-cells,
 CC macrophages, monocytes and/or natural killer cells. Localised
 CC prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal.
 SQ Sequence 255 AA.

Query Match 99.8%; Score 1760; DB 1; Length 255;
 Best Local Similarity 99.6%; Pred. No. 9.88e-145;
 Matches 238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 17 ESQPDKPELHKSSKFTGLMNMKVLVDNHNVAIVKSIDQFLFYDLIYSIKDKLGN 76
 |||
 OY 1 ESQPDKPELHKSSKFTGLMNMKVLVDNHNVAIVKSIDQFLFYDLIYSIKDKLGN 60
 DB 77 YDNVREFFKNKDLADYKXKYVDVFGANYYYOCYFSKKTNDINSHTDKRCKTMGCVTE 136
 |||
 OY 61 YDNVREFFKNKDLADYKXKYVDVFGANYYYOCYFSKKTNDINSHTDKRCKTMGCVTE 120
 DB 137 HNGNQLDKRSTIVRFEDEGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 196
 |||
 OY 121 HNGNQLDKRSTIVRFEDEGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 DB 197 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLAMYNDNKWVDSKDVKIEVYLTTRKK 255
 |||
 OY 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLAMYNDNKWVDSKDVKIEVYLTTRKK 239

RESULT 3
 ID R13206 standard; Protein: 239 AA;
 AC R13206;
 DT 15-OCT-1991 (first entry)
 DE Staphylococcal enterotoxin B.

KW SEB; cancer treatment; pyrogen; tumouricide.
 OS Staphylococcus aureus.
 PN M09110680-A.
 PD 25-JUL-1991.
 PF 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 PS Disclosure; Fig 1; 74pp; English.
 CC SEB was isolated and purified from S. aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEB. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydropathy profiles.
 CC See R13203-R13211.
 SQ Sequence 239 AA.

Query Match 97.8%; Score 1725; DB 1; Length 239;
 Best Local Similarity 97.9%; Pred. No. 1.44e-141;
 Matches 234; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 1 ESQPDKPELHKSSKFTGLMNMKVLVDNHNVAIVKSIDQFLFYDLIYSIKDKLGN 60
 |||
 OY 1 ESQPDKPELHKSSKFTGLMNMKVLVDNHNVAIVKSIDQFLFYDLIYSIKDKLGN 60
 DB 61 YDNVREFFKNKDLADYKXKYVDVFGANYYYOCYFSKKTNDINSHTDKRCKTMGCVTE 120
 |||
 OY 61 YDNVREFFKNKDLADYKXKYVDVFGANYYYOCYFSKKTNDINSHTDKRCKTMGCVTE 120
 DB 121 HNGNQLDKRSTIVRFEDEGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 |||
 OY 121 HNGNQLDKRSTIVRFEDEGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 DB 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLAMYNDNKWVDSKDVKIEVYLTTRKK 239
 |||
 OY 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLAMYNDNKWVDSKDVKIEVYLTTRKK 239

RESULT 4

ID R45014 standard; Protein: 239 AA.
 AC R45014;
 DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SEB.
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 OS autoimmune disease; toxicity; Protein A; pertussis system.
 PN M09324136-A.
 PD 09-DEC-1993.
 PF 01-JUN-1993; U05213.
 PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 PI Stone JL, Terman DS;
 DR WPI: 93-405418/50.
 PT use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PS disclosure; Fig 1; 90pp; English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the protein A pertussis system. They may be administered
 CC by i.v. injection.

Seq	Sequence	239 AA:
50	Query Match Best Local Similarity 97.8%; Matches 234; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	Score 1725; DB 1; Length 239; Pred. No. 1,44e-141;
Db	1 ESQDPKPEDELHKSSKFTGLMENKKVLYLDNHNVAIVKSIDQFLYDLIYSIKDIKLG 60	
Qy	1 ESQDPKPEDELHKSSKFTGLMENKKVLYLDNHNVAIVKSIDQFLYDLIYSIKDIKLG 60	
Db	YDNRVFEKKNKDLADKKDKYVDVFGANNYYQCFESKKTNDINSHQDRKRTCMYGGVTE 120	
Qy	YDNRVFEKKNKDLADKKDKYVDVFGANNYYQCFESKKTNDINSHQDRKRTCMYGGVTE 120	
Db	121 HNGNQLDKRSLTYRVFEDGKNLSPDVQTKKKVTYAOELDYLRHLYVKKKLYEFNNS 180	
Qy	121 HNGNQLDKRSLTYRVFEDGKNLSPDVQTKKKVTYAOELDYLRHLYVKKKLYEFNNS 180	
Db	181 PFETGYIKFIFENENSFWYDLMAPAGDKRFDOSKYLMYNTNDKMKVDSKDYKTEVYLTTRKK 239	
Qy	181 PFETGYIKFIFENENSFWYDLMAPAGDKRFDOSKYLMYNTNDKMKVDSKDYKTEVYLTTRKK 239	
RESULT	5	
ID	R45015 standard; protein; 239 AA.	
AC	R45015;	
DT	08-JUN-1994 (first entry)	
DE	Staphylococcal enterotoxin SE1.	
KW	Staphylococcal enterotoxin; SE; cancer; tumouricidal agent; autoimmune disease; toxicity; Protein A; pertussin system.	
OS	Staphylococcus aureus.	
PN	MO9324136-A.	
PD	09-DEC-1993.	
PF	01-JUN-1993; 005213.	
PR	01-JUN-1992; US-891718.	
PA	(STON.) STONE J L.	
PI	(TERM.) TERMAN D S.	
DR	Stone JL, Terman DS;	
PT	WPI: 93-405418/50.	
PT	Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune diseases	
PT	Disclosures: Fig 1; 90pp; English.	
PS	The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs) which may be used in the methods of the invention for treating cancer in a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A pertussin system. They may be administered by i.v. injection.	
CC	by i.v. injection.	
CC	Sequence 239 AA;	
Seq	Query Match	66.7%; Score 1176; DB 1; Length 239;
	Best Local Similarity 66.4%; Pred. No. 3.93e-92;	
	Matches 160; Conservative 41; Mismatches 34; Indels 6; Gaps 6;	
Db	1 ESQDPKPEDELHKSSKFTGLMENKKVLYLDNHNVAIVKSIDQFLYDLIYSIKDIKLG 60	
Qy	1 ESQDPKPEDELHKSSKFTGLMENKKVLYLDNHNVAIVKSIDQFLYDLIYSIKDIKLG 60	
Db	YDNRVFEKKNKDLADKKDKYVDVFGANNYYQCFESKKTNDINSHQDRKRTCMYGGVTE 120	
Qy	YDNRVFEKKNKDLADKKDKYVDVFGANNYYQCFESKKTNDINSHQDRKRTCMYGGVTE 120	
Db	121 HNGNQLDKRSLTYRVFEDGKNLSPDVQTKKKVTYAOELDYLRHLYVKKKLYEFNNS 180	
Qy	121 HNGNQLDKRSLTYRVFEDGKNLSPDVQTKKKVTYAOELDYLRHLYVKKKLYEFNNS 180	
Db	181 PFETGYIKFIFENENSFWYDLMAPAGDKRFDOSKYLMYNTNDKMKVDSKDYKTEVYLTTRKK 239	
Qy	181 PFETGYIKFIFENENSFWYDLMAPAGDKRFDOSKYLMYNTNDKMKVDSKDYKTEVYLTTRKK 239	

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QY      238      K 238

RESULT      6
ID      R13207 standard; Protein; 239 AA.
AC      R13207;
DE      15-OCT-1991 (first entry)
DE      Staphylococcal enterotoxin C1.
KW      SECL: cancer treatment; pyrogen; tumouricide.
OS      Staphylococcus aureus.
PN      W09110680-A.
PD      25-JUL-1991.
PR      17-JAN-1991; U00342.
PR      17-JAN-1990; US-466577.
PA      (TERM/) TERMAN D S.
PI      Terman DS;
DR      WPI: 91-237984/32.
PR      Treating cancer with enterotoxin from Staphylococcus aureus -
PR      administered by IV injection, having same tumoricidal activity
PS      as Staphylococcal protein A without potential toxic reactions
PS      Disclosure: Fig 1; 74pp. English.
CC      SECL was isolated and purified from S.aureus. It can be used for
CC      treating cancer, activating cytokine mediators and procoagulant
CC      systems, augmenting natural killer cell cytotoxicity, etc. The
CC      enterotoxin can be administered intravenously, optionally with
CC      ibuprofen to attenuate toxic reaction to SECL. Synthetic
CC      polypeptides having structural homology to Staphylococcal exotoxins
CC      are claimed, provided the homology includes statistically
CC      significant sequence homology, alignment of cysteine residues and
CC      similar hydropathy profiles.
CC      See R13203-R13211.
SQ      Sequence      239 AA;

Query Match      66.7%; Score 1176; DB 1; Length 239;
      Best Local Similarity 66.4%; Pred. NO. 3,93e-92;
      Matches 160; Conservativity 41; Mismatches 34; Indels 6; Gaps 6;

Db      1 ESQPPPTDELLHKASKKFTGLMKNKVLVDHIVYSATKYKSVDRFLADHLINISDKLKN 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1 ESQPPPKDELHKSSKFTGLMKNKVLVDHNVSHINKSIDOFLYFDLITISIDTRLGN 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 YDKVTELLNEGLAKKYDEVVDVYGSNNYVNCYFSSK-DNV-SKVYGG-KTCMYGKITK 117
      ||||| :| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|
QY      61 YDNVAVERRKNNDLADKXYDKYDVFAGNYYVQCFFSKTNDINSHEDDKRITCYGGVTE 120
      ||||| :| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|
Db      118 HEGHFHDNGNLQNLVILIRYENKRNITSEFVOTDKKSVTAOELDIKARNFLINKNLVEFN 177
      ||||| :| :| ||||| :| :| ||||| ||||| ||||| ||||| ||||| ||||| :|
QY      121 HNGNOLDK-Y-RSLIVRYEEDGKNLISFDVOTNNKKYTAOELDYLTIRHYLVKNNKLYEFN 178
      ||||| :| :| ||||| :| :| ||||| ||||| ||||| ||||| ||||| ||||| :|
Db      178 SSPYTGIRKIFLNNGNFWDLPAPEDKRDQSKYLLMAYNDKNTVYQSKYIEVHLJTTK 237
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      179 NSPIYTGIRKIFLNE-NSFWIDMPAPEDKRDQSKYLLMAYNDKNTVYQSKYIEVLYTTK 237
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db      238      N 238
QY      238      K 238

RESULT      7
ID      R45016 standard; protein; 238 AA.
AC      R45016;
DE      08-JUN-1994 (first entry)
DE      Staphylococcal enterotoxin SEC3.
KW      Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW      autoimmune disease; toxicity; Protein A; perfusion system.
OS      Staphylococcus aureus.
PN      W09324136-A.
PD      09-DEC-1993.
PR      01-JUN-1993; U05213.
PR      01-JUN-1992; US-891718.
PA      (STON/) STONE J L.
PA      (TERM/) TERMAN D S.

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PT Preventing or treating toxic effects of super antigens - by admn. of
PT new modified or mutated super antigen which induces antibodies but
PT not T-cell activation
PS Disclosure: Fig 3: 54pp; 2013
CC The sequences given in R4190-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (Sag). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by Sag that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;
SQ

Query Match 42.9%; Score 756; DB 1; Length 190;
Best Local Similarity 58.9%; Pred. No. 1.09e-54;
Matches 112; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

Dd 1 ESQDPKPEDELHKSSKFTGLMENKKVLYLDHNVSAIVKSIDQFLYFDLIYSIKDTLKG 60
Qy 1 ESQDPKPEDELHKSSKFTGLMENKKVLYLDHNVSAIVKSIDQFLYFDLIYSIKDTLGN 60
Dd 61 YDNVRFVEKKNLDADKYKDKYVDVFGANYYYQCYFSNNNNNNNNNNNNNNNNNNNNNN 120
Qy 61 YDNVRFVEKKNLDADKYKDKYVDVFGANYYYQCYFSKKTNDINSHFDKRTCTGCGVTE 120
Dd 121 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180
Qy 121 HNGNQDLKRSITVRFVEDGKNLLSFDQGTNRKKKVTQAQELDYLTRHLYLVKNNKILYEFNNS 180

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QY	181	PFETGYIKFI	190
RESULT	12		
ID	R41993	standard; protein; 190	AA.
AC	R41993:		
DT	21-APR-1994	(first entry)	
DE	Staphylococcus enterotoxin B mutant BR-291.		
KW	Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;		
KW	random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;		
KW	autoimmune disease.		
OS	Staphylococcus aureus.		
FT	Key	location/Qualifiers	
FT	region	97..157	
FT		/note="Region undisclosed in the specification"	
FT	region	162..186	
FT		/note="Region undisclosed in the specification"	
FN	W09314634-A.		

FR 28-JAN-1993; 000635Z.
 PR 28-JAN-1992; US-827540.
 PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 PI KAPPLER JW, MARRACK P;
 DR MPI: 93-320314/40.
 PT Preventing or treating toxic effects of super antigens - by admin. of
 PT not modified or mutated super antigen which induces antibodies but
 PT not T-cell activation
 PS Disclosure: Fig 3; 54pp; English.
 CC The sequences given in RA190-2013 are mutant versions of the
 CC *Staphylococcus enterotoxin B* (SEB) super antigen (Sag). These mutants
 CC generated by random mutation by PCR, may be used to modify the T-cell
 CC response elicited by an antigen, by interacting with specific Vbeta
 CC elements of the T-cell receptors. This T-cell response modulation
 CC may be useful in a wide variety of autoimmune diseases, where self-
 CC reactive T-cells may be activated by Sag that bind to particular
 CC Vbeta types.
 CC Sequence 190 AA;
 Query Match 42.9%; Score 756; DB 1; Length 190;
 Best Local Similarity 58.9%; Pred. No. 1.09e-54;
 Matches 112; Conservative 30; Mismatches 48; Indels 0; Gaps 0

Db 1 ESQPDPRDELHSSKFTGLMESMKVLYDNDHVSAINVKSIDDFLYDLISIKDKTLGN 60
1 ESQPDPRDELHSSKFTGLMESMKVLYDNDHVSAINVKSIDDFLYDLISIKDKTLGN 60
Qy 61 YDVRVVEFKKKDLADKKYKDYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
61 YDVRVVEFKKKDLADKKYKDYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
Qy 121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Db 121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Qy 181 PYETGYIKFI 190
181 PYETGYIKFI 190

RESULT 13
ID R41996 standard; protein: 190 AA.
AC R41996;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BC-88.
KW Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
autoimmune disease.
OS Staphylococcus aureus.
FH key Location/Qualifiers
FT region 97..157
FT /note= "Region undisclosed in the specification"
FT 162..186
FT /note= "Region undisclosed in the specification"
PD MO9314634-A.
PN 05-AUG-1993.
PR 28-JAN-1992; US-827540.
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Kappler JM, Marrack P;
DR MPI; 93-320314/40.
PT Preventing or treating toxic effects of super antigens - by admin. of
new modified or mutated super antigen which induces antibodies but
not T-cell activation
PS Disclosure; Fig 3; 54pp; English.
CC The sequences given in R41990-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by SAg that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;

Query Match 42.9%; Score 756; DB 1; Length 190;
Best Local Similarity 58.9%; Pred. No. 1.09e-54;
Matches 112; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

Db 1 ESQPDPRDELHSSKFTGLMESMKVLYDNDHVSAINVKSIDDFLYDLISIKDKTLGN 60
1 ESQPDPRDELHSSKFTGLMESMKVLYDNDHVSAINVKSIDDFLYDLISIKDKTLGN 60
Qy 61 YDVRVVEFKKKDLADKKYKDYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
61 YDVRVVEFKKKDLADKKYKDYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
Qy 121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Db 121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Qy 181 PYETGYIKFI 190
181 PYETGYIKFI 190

RESULT 14
ID R41992 standard; protein: 190 AA.
AC R41992;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BR-257.
KW Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
autoimmune disease.
OS Staphylococcus aureus.
FH key Location/Qualifiers
FT region 97..157
FT /note= "Region undisclosed in the specification"
FT 162..186
FT /note= "Region undisclosed in the specification"
PD MO9314634-A.
PN 05-AUG-1993.
PR 28-JAN-1992; US-827540.
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Kappler JM, Marrack P;
DR MPI; 93-320314/40.
PT Preventing or treating toxic effects of super antigens - by admin. of
new modified or mutated super antigen which induces antibodies but
not T-cell activation
PS Disclosure; Fig 3; 54pp; English.
CC The sequences given in R41990-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by SAg that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;

Query Match 42.8%; Score 755; DB 1; Length 190;
Best Local Similarity 58.4%; Pred. No. 1.34e-54;
Matches 111; Conservative 31; Mismatches 48; Indels 0; Gaps 0;

Db 1 ESQPDPRDELHSSKFTGLMESMKVLYDNDHVSAINVKSIDDFLYDLISIKDKTLGN 60
1 ESQPDPRDELHSSKFTGLMESMKVLYDNDHVSAINVKSIDDFLYDLISIKDKTLGN 60
Qy 61 YDVRVVEFKKKDLADKKYKDYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
61 YDVRVVEFKKKDLADKKYKDYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
Qy 121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Db 121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
121 HNGNQDLKYSITVRVFEDEKKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Qy 181 PYETGYIKFI 190
181 PYETGYIKFI 190

RESULT 15
ID R42000 standard; protein: 190 AA.
AC R42000;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BA-15.
KW Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
autoimmune disease.
OS Staphylococcus aureus.
FH key Location/Qualifiers
FT region 97..157
FT /note= "Region undisclosed in the specification"
FT 162..186
FT /note= "Region undisclosed in the specification"
PD MO9314634-A.
PN 05-AUG-1993.

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 WISE (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 20 15:08:07 2000; MasPar time 15.27 Seconds
 Tabular output not generated. 467,552 Million cell updates/sec

Title: >US-09-150-947-12
 Description: (1-239) from US09150947.pep
 Perfect Score: 1763
 Sequence: 1 ESQPPDKPDELHKSSKFTGL.....NKAVDSKDKVIEVYLTTKK 239

Scoring table:
 PAM 150
 Gap 11

Searched: 82229 segs, 29864866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 47.318; Variance 95.221; scale 0.497

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1760	99.8	266	1	ETXB_STPAU ENTEROTOXIN TYPE B PRE	0.00e+00
2	1183	67.1	266	1	ETC1_STPAU ENTEROTOXIN TYPE C-1 P	1.67e-210
3	1156	65.6	266	1	ETC3_STPAU ENTEROTOXIN TYPE C-3 P	6.66e-205
4	1148	65.1	266	1	ETC2_STPAU ENTEROTOXIN TYPE C-2 P	3.03e-203
5	746	42.3	251	1	SPEA_STRPY EXOTOXIN TYPE A PRECUR	1.08e-120
6	412	23.4	258	1	ETXD_STPAU ENTEROTOXIN TYPE D PRE	2.16e-54
7	375	21.3	257	1	ETXE_STPAU ENTEROTOXIN TYPE E PRE	1.15e-38
8	329	18.7	257	1	ETXE_STPAU ENTEROTOXIN TYPE E PRE	6.04e-10
9	165	9.4	235	1	SPEC_STRPY EXOTOXIN TYPE C PRECUR	3.24e-02
10	112	6.4	517	1	CP5H_CANTR CYTOCHROME P450 52A8	3.24e-02
11	105	6.0	796	1	DECI_YEAST DECI PROTEIN (MDM2 PR	2.56e-01
12	106	6.0	1328	1	YME4_YEAST TRANSPOSIN TY1 PROTEIN	1.92e-01
13	106	6.0	1328	1	YMD9_YEAST TRANSPOSIN TY1 PROTEIN	1.92e-01
14	106	6.0	1328	1	YMD9_YEAST TRANSPOSIN TY1 PROTEIN	1.92e-01
15	105	6.0	1347	1	YCB9_YEAST TRANSPOSIN TY1-17 PROT	2.56e-01
16	106	6.0	1755	1	YJZ7_YEAST TRANSPOSIN TY1 PROTEIN	1.92e-01
17	105	6.0	1755	1	YJZ9_YEAST TRANSPOSIN TY1 PROTEIN	2.56e-01
18	104	5.9	638	1	GLE_CHLRE AUTOLYSIN PRECURSOR (E	3.42e-01
19	104	5.9	722	1	Y290_HAEN PROBABLE CATION-TRANS	3.42e-01
20	104	5.9	1328	1	YMT5_YEAST TRANSPOSIN TY1 PROTEIN	3.42e-01
21	104	5.9	1409	1	CPM1_DROME COPA PROTEIN	3.42e-01
22	102	5.8	342	1	YMI2_YEAST HYPOTHETICAL 39.2 KD P	6.05e-01
23	103	5.8	500	1	Y039_BORBU HYPOTHETICAL PROTEIN B	4.55e-01

24	102	5.8	776	1	ARCB_ECOLI AEROBIC RESPIRATION CO	6.05e-01
25	103	5.8	918	1	CAPP_CORGL PHOSPHOENOLPYRUVATE CA	4.55e-01
26	98	5.6	131	1	SP27_CABEL SPERMATOCYTE PROTEIN S	1.85e+00
27	99	5.6	321	1	VG16_BPB03 ENCAPSIDATION PROTEIN	1.40e+00
28	97	5.5	404	1	TY3H_CABEL PUTATIVE TYROSINE 3-MO	2.43e+00
29	97	5.5	605	1	ETFI_FOMP1 EARLY TRANSCRIPTION FA	2.43e+00
30	97	5.5	682	1	REGC_BACSU ATP-DEPENDENT DNA HELI	2.43e+00
31	97	5.5	710	1	PAL3_PHAVU PHENYLALANINE AMMONIA-	2.43e+00
32	97	5.5	2090	1	N214_HUMAN NUCLEAR PORE COMPLEX P	2.43e+00
33	97	5.5	2314	1	PPT2_HUMAN PROTEIN-TYROSINE PHOSP	2.43e+00
34	97	5.4	666	1	VOO1_VARV PROTEIN O1	3.19e+00
35	95	5.4	1476	1	CFTR_MOUSE CYSTIC FIBROSIS TRANSM	4.18e+00
36	96	5.4	2316	1	PTP2_RAT PROTEIN-TYROSINE PHOSP	3.19e+00
37	94	5.3	464	1	GATH_YEAST PROBABLE GLUTAMYL-TRNA	5.45e+00
38	94	5.3	519	1	CP53_CANMA CYTOCHROME P450 52A10	5.45e+00
39	94	5.3	519	1	CP5K_CANMA HYPOHETICAL 63.9 KD P	7.11e+00
40	93	5.3	560	1	YJRS_YEAST PROTEIN-TYROSINE PHOSP	7.11e+00
41	93	5.3	700	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
42	94	5.3	971	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
43	94	5.3	986	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
44	94	5.3	1476	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
45	93	5.3	1682	1	MSPI_PLAF3 MEROZOITE SURFACE PROT	7.11e+00

ALIGNMENTS

RESULT ID	1	STANDARD	PRT	266 AA.
AC	ETXB_STPAU			
AC	P01552;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENTEROTOXIN TYPE B PRECURSOR (SEB).			
GN	ENTB.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
CC	Bacillus/Staphylococcus group; Staphylococcus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 86168029.			
RA	JONES C.L., KHAN S.A.;			
RT	"Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.";			
RT	aureus.";			
RL	[1]. Bacteriol. 166:29-33(1986).			
RN	[2]			
RP	SEQUENCE OF 40-91 FROM N.A.			
RX	MEDLINE: 85298255.			
RA	RANELLI D.M., JONES C.L., JOHNS M.B., MUSEY G.J., KHAN S.A.;			
RT	"Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).			
RN	[3]			
RP	SEQUENCE OF 28-266 (S-6).			
RX	MEDLINE: 71007902.			
RA	HUANG I.-Y., BERGDOHL M.S.;			
RT	"The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";			
RT	J. Biol. Chem. 245:3518-3525(1970).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).			
RX	MEDLINE: 93063291.			
RA	SWAMINATHAN S., FOREY W.F. JR., PLETCHER J., SAX M.;			
RT	"Crystal structure of staphylococcal enterotoxin B, a superantigen.";			
RT	Nature 359:801-806(1992).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.			
RX	MEDLINE: 94203282.			
RA	JARETZKY T.S., BROWN J.H., GORCA J.C., STERN L.J., URBAN R.G.,			
RA	CHI Y.I., STAUFFACHER C., STROMINGER J.L., WILEY D.C.;			
RT	"Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";			
RT	Nature 368:711-718(1994).			

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RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE: 99096298.
RA LI H., LIERA A., TSUCHIYA D., LEDER L., YSERN X., SCHLIEVERT P.M.,
RA KARJALAINEN K., MARIUTZA R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN [77]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE: 98181012.
RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC PRESENSE STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
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CC -----
DR EMBL: M1118; AAA8550.1; -.
DR PIR: A01815; ENSAB6.
DR PIR: S27360; S27360.
DR PDB: 1SEB: 20-JUN-96.
DR PDB: 2SEB: 28-JAN-98.
DR PDB: 3SEB: 27-MAY-98.
DR PDB: 1SE3: 16-JUN-97.
DR PDB: 1SE4: 15-OCT-97.
DR PDB: 1SBB: 04-MAR-99.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_Toxin; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT CHAIN 1 27
FT SIGNAL 28 266
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
SQ SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;
Query Match 99.8%; Score 1760; DB 1; Length 266;
Best Local Similarity 99.6%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;
Matches 238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 208 PYETGYIKFIENENSWFWDMPAPGDKFDQSKYLMYNDKNDKVDKYLEVLTTRKK 266
OY 181 PYETGYIKFIENENSWFWDMPAPGDKFDQSKYLMYNDKNDKVDKYLEVLTTRKK 239
RESULT 2
ID ETC1_STAUB STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88038352.
RA BOBACH G.A., SCHLIEVERT P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE: 83213327.
RA SCHMIDT J.J., SPERO L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC -----
DR EMBL: X05815; CAA29260.1; -.
DR PIR: A01816; ENSAC1.
DR PIR: S06356; S06356.
DR HSSP: P34071; 1SE2.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_Toxin; 1.
KW Enterotoxin; Toxin; Signal; Superantigen.
FT CHAIN 1 27
FT SIGNAL 28 266
FT DISULFID 120 137
FT CONFLICT 177 177
SQ SEQUENCE 266 AA; 30546 MW; FE00255A CRC32;
Query Match 67.1%; Score 1183; DB 1; Length 266;
Best Local Similarity 66.8%; Pred. No. 1.67e-210; Mismatches 34; Indels 6; Gaps 6;
Matches 161; Conservative 40; Mismatches 34; Indels 6; Gaps 6;

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OY 179 NSPYETGYIKFIENE-NSFWYDMMPAPGDKFPQSKYLMYNDNKVDSKDVXIEVYLTFR 237
DB 265 N 265
OY 238 K 238

RESULT 3
ID ETC3_STRAU STANDARD: PRT: 266 AA.
AC P2313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
GN ENTC3.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
RN Bacillus/Staphylococcus group; Staphylococcus.
  [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90220508.
RA HOVDE C.J., HACKETT S.P., BOHACH G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins."
RL Mol. Gen. Genet. 220:329-333(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECEPTOR.
RX MEDLINE: 97064178.
RA FIELDS B.A., MALCHIODI E.L., LI H., YSEEN X., STAUFACHER C.V.,
RA SCHLIEVERT P.M., KARJALAINEN K., MARIUZZA R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen."
RL Nature 384:188-192(1996).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PIROGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC -----
DR EMBL: X51661; CA35972.1; -.
DR PIR: S11885; S11885.
DR PDB: 1UCR; 12-NOV-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFMW: PF01123; Staph_Strep_toxin; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137 BY SIMILARITY.
SQ SEQUENCE 266 AA; 30671 MW; 27B4DD0A CRC32;

Query Match 65.6%; Score 1156; DB 1; Length 266;
Best Local Similarity 66.0%; Pred. No. 6,66e-205;
Matches 135; Conservative 40; Mismatches 36; Indels 6; Gaps 6;
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OY 121 HNGNDLDR-Y-RSIVRVFEDSKNLISFVQFNKKRYTQEDLDYLRHLVKNKKRIEYN 178
DB 205 SSPYETGYIKFIENNNGNFWYDMMPAPGDKFPQSKYLMYNDNKVDSKSVXIEVHLTFR 264
OY 179 NSPYETGYIKFIENE-NSFWYDMMPAPGDKFPQSKYLMYNDNKVDSKDVXIEVYLTFR 237
DB 265 N 265
OY 238 K 238

RESULT 4
ID ETC3_STRAU STANDARD: PRT: 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ENTC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
RN Bacillus/Staphylococcus group; Staphylococcus.
  [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE: 89277549.
RA BOHACH G.A., SCHLIEVERT P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2."
RL Infect. Immun. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE: 96027099.
RA PAPAGEORGIOU A.C., ACHARYA K.R., SHAPIRO R., PASSALACQUA E.F.,
RA BREHM R.D., TRANTER H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT staphylococcus aureus reveals a zinc-binding site."
RL Structure 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE: 96022987.
RA SWAININTHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE: 9734373.
RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PIROGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
DR PIR: A60114; A60114.
DR PDB: 1STE; 23-DEC-96.
DR PDB: 1SE2; 08-MAR-96.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFMW: PF01123; Staph_Strep_toxin; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; A15FD37 CRC32;
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Query Match Similarity 65.1%; Score 1148; DB 1; Length 266;
Best Local Similarity 65.6%; Pred. No. 3.03e-203;
Matches 138; Conservative 40; Mismatches 37; Indels 6; Gaps 6;

Db      ESOPDPPEDELKSSSEFTGTGMGNMKLYDDHYVSAATKVASVYKFLAHLADIYINISPKLKN 87
Oy      1 ESOPDPPEDELKSSSEFTGTGMGNMKLYDDHYVSAATKVASVYKFLAHLADIYINISPKLKN 60
Db      88 YDKVTELLINEDLAKKYKDEYVDYGSNTYNYVCYSSK-DNV-KGYTGG-KTCMTGCTIK 144
Oy      61 YNNVREEFNKKDLADKYKDYVDVGANYCYCSKSKTNDINSHETDRKTCMGVGYTE 120
Db      145 HGHNEHDNCLNQLIRYVENKRNITSEFVQVDKDSVTAQOELDIARNLILKKNLYEN 204
Oy      121 HNGNOLDK-Y-ISTYRVDEDEKNNLSFVQYNNKKVTAQOELDYLRHLYVNNKLYEYFN 178
Db      205 SSPETGYIKFLIENNGNTFPMYDMPAPGPKFOSKILMYNNKTYVDSVYIEVHLTRK 264
Oy      179 NSPYEGYIKFLIENE-NSPYDMPAPGPKFOSKILMYNNKTYVDSVYIEVHLTRK 237
Db      265 N 265
Oy      238 K 238

RESULT      5
ID      SPEA-STIRPY      STANDARD:      PRT;      251 AA.
*AC      P08095;
DT      01-AUG-1988 (rel. 08, Created)
DT      01-JAN-1990 (rel. 13, Last sequence update)
DT      15-DEC-1998 (rel. 37, Last annotation update)
DE      EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
DE      (SPE A).
GN      SPEA.
OS      Streptococcus pyogenes.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC      Streptococcus.
RN      [1]
RA      SEQUENCE FROM N.A.
RA      MEDLINE; 86166804.
RA      WEEKS C.R., FERRETTI J.J.;
RT      "Nucleotide sequence of the type A streptococcal exotoxin
RT      (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT      T12."
RL      Infect. Immun. 52:144-150(1986).
RL      [2]
RN      RP
RN      SEQUENCE FROM N.A.
RX      MEDLINE; 86284313.
RA      JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
RT      "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT      related to Staphylococcus aureus enterotoxin B."
RL      Mol. Gen. Genet. 203:354-356(1986).
CC      -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC      THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC      FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC      DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC      FEVER.
CC      -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC      -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYROGENES
CC      PYROGENIC EXOTOXINS ARE ALL RELATED.
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CC      -----
DR      EMBL; U04053; AAC48868.1; -
DR      EMBL; X03929; CA22568.1; -
DR      PIR; A26152; A26152.
DR      PIR; S29659; S29659.

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ID	ENTRY	STRAIN	STANDARD	PRG	256 AA
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	ENTEROTOXIN TYPE D PRECURSOR (SED).				
GN	ENTD.				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;				
OC	Bacillus/Staphylococcus group; Staphylococcus.				
RN	1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 89359112.				
RA	BAILES K.W., IANDOLA J.J.;				
RT	"Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.";				
RL	J. Bacteriol. 171:4799-4806(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).				
RC	STRAIN-ATCC 23235;				
RX	MEDLINE; 97157473.				
RA	SUNDSTROM M., ABRAHSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,				
RT	DOHLSTEIN M.;				
RL	"The crystal structure of staphylococcal enterotoxin type D reveals Zn ²⁺ -mediated homodimerization.";				
RL	EMBO J. 15:6832-6840(1996).				
CC	-1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.				
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION				
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.				
CC	-1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES				
CC	PROGENIC EXOTOXINS ARE ALL RELATED.				

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CC DR EMBL; M28521; AAB06195.1; .
CC DR PIR; A33953; A33953.
CC DR HSSP; P13163; ISXT.
CC DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC DR PFAM; PF01123; Staph_Strep_toxin; 1.
CC KW Enterotoxin; Toxin; Signal; Superantigen; Zinc.
CC FT SIGNAL 1 25
CC FT CHAIN 26 258 ENTEROTOXIN TYPE D.
CC FT METAL 212 212 ZINC.
CC FT METAL 250 250 ZINC.
CC FT METAL 252 252 ZINC.
CC FT VARIANT 114 114 P->A (IN STRAIN ATCC 23235).
CC SQ SEQUENCE 258 AA; 29746 MM; 2D1AA120 CRC32;

Query Match 23.4%; Score 412; DB 1; Length 258;
Best Local Similarity 36.6%; Pred. No. 2,16e-54;
Matches 87; Conservative 53; Mismatches 79; Indels 19; Gaps 13;

Db 33 KEKEHKHSESTPLNMNKHSHYADKNPIIGENKSGOFLNTLLKKFFDLNFEDL 92
| |||| : :::: |||| | : : : : |||| : || : ||:::
Qy 7 KPDEIHKSSKTGL-MEMNKVLYTD-NHVSAINAKSIDOFLFDLTYSIKDKLGANYNV 64
93 LINFNSKEMAQHFKSKNVDPYRISINCY-G---GEI-----D-RITAGYGAVPHBGN 142
65 RVEFNRKDLDKDYDVFGANGYYGYCPSKKNNDINSHTDRKTCMGVTLEHNGN 124
Db 143 KLEKKKTPINDMINGVOKEYSLDKVCOTDKKNVYOELDAQRRYLQDKLYNNDTLGG 202
125 QLDKYRSITVRFEDEG-KNLISFD-VQTNKRKKVPQOEIDLYLRHYLVNKKRIYEFPNN-SP 181
Db 203 KIQRKIFEDSDGSKVSYDLFDVGD-FPE-KOLRIYSDNKKTSTEHLHIDIYEXK 258
182 -YECYCTFIETIENENS-FWYDMAPAPGDFDOSKYLMATYNDNMKNADSKOVKEIVLTTR 237

RESULT 7
ID EXTRA STAU STANDARD; PTR; 257 AA.
AC P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE A PRECURSOR (SEA).
GN ENTA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PRI337;
RX MEDLINE; 88086892.
RA BETLEY M.J., MERALANOS J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41(1988).
RN [2]
RP SEQUENCE OF 25-257.
RX MEDLINE; 87222293.
RA HUANG I.-Y., HUGHES J.L., BERGDOLL M.S., SCHANTZ E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE; 95354648.
RA SCHAD E.M., ZAITSEVA I., ZAITSEV V.N., DOHLSTEN M., KALLAND T.,
RA SCHLIEVERT P.M., OHLENDORF D.H., SVENSSON L.A.;

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RT      "Crystall structure of the superantigen staphylococcal enterotoxin
RT      type A." ;
RL      EMBO J. 14 :3292-3301(1995).
RN      [4]
RP      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX      MEDLINE: 97113025.
RA      SUNDTROEM M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEIN M.,
RA      ABRAHAMSEN L.;
RT      "The Co-crystal structure of staphylococcal enterotoxin type A with
RT      zn2+ at 2.7-A resolution. Implications for major histocompatibility
RT      complex class II binding.";
RL      J. Biol. Chem. 271:32212-32216(1996).
RN      [5]
RP      3D-STRUCTURE MODELING.
RX      MEDLINE: 96022987.
RA      SSMAMINTHAN S., FUREX W.F. JR., PLETCHER J., SAX M.;
RT      "Residues defining V beta specificity in staphylococcal
RT      enterotoxins." ;
RN      Nat. Struct. Biol. 2:680-686(1995).
RN      [6]
RP      COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX      MEDLINE: 97334373.
RA      SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., AGHARVA K.R.;
RT      "A structural and functional comparison of staphylococcal
RT      enterotoxins A and C2 reveals remarkable similarity and
RT      dissimilarity." ;
RL      J. Mol. Biol. 269:270-280(1997).
CC      -I- SUBUNIT: MONOMER.
CC      -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC      SYNDROME; STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC      -I- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC      -I- SIMILARITY: THE DIFFERENT S'AUREUS ENTEROTOXINS AND S.PYOGENES
CC      PYOGENIC EXOTOXINS ARE ALL RELATED.
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DR      EMBL; M18970; AAA26681.1; -.
DR      PIR; A28664; A28664.
DR      PIR; A29566; A29566.
DR      PDB; IBSF: 1J-JUN-96.
DR      PDB; 1SEA: 15-OCT-95.
DR      PDB; 1SXT: 18-NOV-97.
DR      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR      PFAM; PF01123; Strep_strep_toxin; 1.
KW      Enterotoxin; Toxin; Signal; Superantigen; zinc; 3d-structure.
FT      SIGNAL          1           24
FT      CHAIN           25          257   ENTEROTOXIN TYPE A .
FT      DISULFID        120         130
FT      METAL            25           25    ZINC.
FT      METAL            211          211    ZINC.
FT      METAL            249          249    ZINC.
FT      METAL            251          251    ZINC.
FT      CONFLICT        242           242    T->S (IN REF. 2) .
SQ      SEQUENCE       257 AA; 29669 MW; D08631B2 CRC32;
Query Match              21.3% Score 375; DB 1; Length 257;
Best Local Similarity    35.0%; Pred No.2,55e-47;
Matches     82; Conservative 56; Mismatches 77; Indels 19; Gaps 12;
Db      Db      35 DLRRKSELQGTALGNKIYYNKEAKTENESHDOFLQHITLFEGFTDHSWYNLDLV 94
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
          10 ELHKSKRTGL-MEMMK-VLYDDNHVSALNVKSIDLQFLFYLLISIKTKGNTDNVAVE 67
          Db      95 FDASKIVRKYGKKVDLYGYATGYOC-----AGC--T'-PKM-TACMGGSVTLDNNRLT 144
          68 EKNDKLARKYDKDYVGANYCYCFSKTYNDINSHEPDKRKTCMYGVTEHGNDLD 127

```

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Db      145 EEKKVPINLMADGKONTVPLETVTKNNKNVTVQELDLQARRYLQEKYKLNYSNVPDGKQ 204
      : : : : | | | : : : | | | | | | | : | | : : : : :
Qy      128 KYSTIVRVFEDSK-NLISD-VQTNKKKVTQAQELDYLRHLYVKKKKLEFNN-NSPYE 183
      : : : : | | | : : : | | | | | | | : | | : : : : :
Db      205 RGLIVHSTEPSVNYDLFGAQO-QSMT-LRIRYDNKNTINSENMHIDLYLT 256
      : : : : | | | : : : | | | | | | | : | | : : : : :
Qy      184 TGXIKF-IEENENFWYDMPAPGDKFDQSKYLMYNDKNKVDKIVIEYLLT 236
      : : : : | | | : : : | | | | | | | : | | : : : : :

RESULT 8
ID      ETRX-STRAU      STANDARD:      PRT:      257 AA.
AC      P12993;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN      ENTE.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group;
OC      Bacillus/Staphylococcus group; Staphylococcus.
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC      STRAIN-MJB265;
RC      MEDLINE; 88257005.
RA      COUCH J.L., SOLTIS M.T., BETLEY M.J.;
RT      "Cloning and nucleotide sequence of the type E staphylococcal
RT      enterotoxin gene.";
RL      J. Bacteriol. 170:2954-2960(1988).
RN      [2]
RP      3D-STRUCTURE MODELING.
RC      MEDLINE; 96022987.
RA      SWAMINATHAN S., FUREY W.F., JR., PLETCHER J., SAX M.;
RT      "Residues defining V beta specificity in staphylococcal
RT      enterotoxins.";
RL      Nat. Struct. Biol. 2:680-686(1995).
CC      -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC      STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC      -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC      PYROGENIC EXOTOXINS ARE ALL RELATED.
CC      -----
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CC      -----
DR      EMBL; M21319; AAA26617.1; -
DR      PIR; A28179; A28179.
DR      PDB; 1SEB; 15-OCT-95.
DR      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR      PFWAM; PF01123; Staph_Strep_toxin; 1.
KW      Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT      SIGNAL 1 27
FT      CHAIN 28 257 ENTEROTOXIN TYPE E.
SQ      SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;

Query Match 18.7%; Score 329; DB 1; Length 257;
Best local Similarity 33.8%; Pred. No. 1,15e-38;
Matches 79; Conservative 56; Mismatches 80; Indels 19; Gaps 13;

Db      35 DLKKSELDQNALSNLRQIYYNEKAITENKESDQFLNTLLFKGFTGHPMYNDLVD 94
      : | | | : : : : | | | | | | | : | | : : : : :
Qy      10 ELHKSSKFT-GLMENMK-VLYDDNHSAIVKSIDQFLYDLIYSIKDTLGYNDVRYE 67
      : | | | : : : : | | | | | | | : | | : : : : :
Db      95 LGSKDKATNKKKKGVLDLYGAYGYOC-----AGS--T--PNK-TACHYGVTLHDNRLT 144
      : : : : | | | | | | | : | | : : : : :
Qy      68 FKKKDLADKRYDYVVEGANYCYFYSKKTNDINSHETDKRRTKYGVGTEHNGQD 127
      : : : : | | | | | | | : | | : : : : :
Db      145 EEKKVPINLMADGKONTVPIDKVTSKKEVTQVELDLQARRYLHKGKGLYNSDPGKQ 204

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Qy      128 KYSTIVRVFEDSKNL-LISD-VQTNKKKVTQAQELDYLRHLYVKKKKLEFNN-SP-YE 183
      : : : : | | | : : : | | | | | | | : | | : : : : :
Db      205 RGLIVHSSGSGSVSYDLFGAQO-YPDT-LRIRYDNKNTINSENMHIDLYLT 256
      : : : : | | | : : : | | | | | | | : | | : : : : :
Qy      184 TGXIKFIEENENS-FWYDMPAPGDKFDQSKYLMYNDKNKVDKIVIEYLLT 236
      : : : : | | | : : : | | | | | | | : | | : : : : :

RESULT 9
ID      SPEC-STREPY      STANDARD:      PRT:      235 AA.
AC      P13380;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      EXOTOXIN TYPE C PRECURSOR (SPE C).
GN      SPEC.
OS      Streptococcus pyogenes.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC      Streptococcus.
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
RC      STRAIN-T18P / MGAS 1585;
RC      MEDLINE; 88314303.
RA      GOSHORN S.C., SCHLIEVERT P.M.;
RT      "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";
RL      Infect. Immun. 56:2518-2520(1988).
RN      [2]
RP      REVISIONS TO 21-26.
RC      STRAIN-T18P / MGAS 1585;
RC      MEDLINE; 92363541.
RA      KAPUR V., NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT      "Molecular population genetic evidence of horizontal spread of two
RT      alleles of the pyrogenic exotoxin C gene (spec) among pathogenic
RT      clones of Streptococcus pyogenes.";
RL      Infect. Immun. 60:3513-3517(1992).
RN      [3]
RP      X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
RC      MEDLINE; 97397352.
RA      ROUSSEL A., ANDERSON B.F., BAKER H.M., FRASER J.D., BAKER E.N.;
RT      "Crystal structure of the streptococcal superantigen SPE-C:
RT      dimerization and zinc binding suggest a novel mode of interaction
RT      with MHC class II molecules.";
RL      Nat. Struct. Biol. 4:635-643(1997).
CC      -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC      THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC      FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC      DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC      FEVER.
CC      -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC      -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC      PYROGENIC EXOTOXINS ARE ALL RELATED.
CC      -----
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CC      -----
DR      EMBL; M35514; AAA27017.1; ALT_SEQ.
DR      EMBL; M97156; AAB59091.1; -
DR      EMBL; M97157; AAB59092.1; -
DR      PIR; A30509; A30509.
DR      PDB; 1AN8; 29-APR-98.
DR      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR      PFWAM; PF01123; Staph_Strep_toxin; 1.
KW      Toxin; Signal; 3D-structure.
FT      SIGNAL 1 27
FT      CHAIN 28 235 EXOTOXIN TYPE C.
SQ      SEQUENCE 235 AA; 27372 MW; 524BB55D CRC32;

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Query Match      9.4%: Score165; DB 1; Length 235;
Best Local Similarity 25.8%; Pred.No. 6 04e-10;
Matches          32; Conservative 37; Mismatches 49; Indels 6; Gaps 6;

Dd   113 IYGGITPAQNNKVN-HKLGLNLFISGESQOMLNKKILEKDIDVFEQIDFKIRKYAMDNY 171
       :|::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
Oy   114 MYGVSVTEHNGNQDLKYSRI-TVWVEFEDCKNLDSFDVGNKKKAKVTQDELDTLRHLVANK 172
Dd   172 KIYD-AIISPVGSGKEIKTDKGHEQIDLFPSPNEG-TRSDIFAKYKNRRIINMKNSHF 229
       |:|:|: ||||: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
Oy   173 KLYEENNPSPEYGYIKFIEENSNF-WYDMMPAPGDGFPOSKXYLMAYNDNKVDYSD-KVI 230
Db    230 DYL 233
Oy     :||
Oy    231 EYVL 234

RESULT 10
ID CP5H.CANTR STANDARD: PRT: 517 AA.
AC P30610;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 52A8 (EC 1.14.14.1) (CYPLIIB8) (ALKANE-INDUCIBLE P450-ALK5).
GN CYP52A8.
OS Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Candidaceae; Candida.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 750;
RX MEDLINE: 93090274.
RA SEGHEZZI W., METILI C., RUFFINER R., KUENZLI R., SANGULARD D.,
RA FIECHTER A.;
RT "Identification and characterization of additional members of the
RT cytochrome P450 multigene family CYP52 of Candida tropicalis.";
RL DNA Cell Biol. 11:767-780(1992).
CC -FUNCTION: TOGETHER WITH AN NADPH CYTOCHROME P450 THE ENZYME SYSTEM
CC CATALYZES THE TERMINAL HYDROXYLATION AS THE FIRST STEP IN THE
CC ASSIMILATION OF ALKANES AND FATTY ACIDS. PREFERENTIALLY
CC HYDROXYLATES LAURIC ACID.
CC -1- CATALYTIC ACTIVITY: HYDROXYLATION OF N-ALKANES AT THE TERMINAL
CC POSITION.
CC -1- INDUCTION: BY VARIOUS ALKANES.
CC CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
-----
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-----
DR EMBL: Z13012; CAJ78356.1; -.
DR PIR: S22974; S22974.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR PFAM: PF00067; P450; 1.
KW Electron transport; Oxidoreductase; Monooxygenase; Heme.
FT BINDING 464 464 HEME (BY SIMILARITY).
SQ SEQUENCE 517 AA; 59525 MW; D851204F CRC32;

Query Match      6.4%: Score 112; DB 1; Length 517;
Best Local Similarity 27.9%; Pred. No. 3 24e-02;
Matches          17; Conservative 20; Mismatches 18; Indels 6; Gaps 5;

Dd   189 FTVDASAEFLFGESVHSKDETIGSYODD-IDFVGRKDFAESFNKAOEYLAIRTLVDDFY 247
       :|:|:|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
Oy   36 INVNSIDQFLVFDDLITSIKDKTRLGYNVDNVRYEFKN-KDLADKY-YVDV--EGANY 90
Db    248 Y 248
       |

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Yy	91 Y	91
RESULT	11	
ID	DEC1_YEAST	STANDARD;
AC	012387;	PRT;
DT	01-NOV-1997 (Rel. 35, Created)	796 AA.
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DE	DEC1 PROTEIN (MDM20 PROTEIN).	
GN	DEC1 OR MDM20 OR YOL076W.	
OS	Saccharomyces cerevisiae (Baker's yeast).	
OC	Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;	
CC	Saccharomycetaceae; Saccharomyces.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	KINGSBURY T.J., HOYT M.A.;	
RL	Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	HERMANN G.J., SHAW J.M.;	
RL	Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 97321807.	
RA	TEREMTA M., KATSIOULOU C., ALEXANDRAKI D.;	
RT	"Sequence analysis of a 33.2 kb segment from the left arm of yeast	
RT	chromosome XV reveals eight known genes and ten new open reading	
RT	frames including homologues of ABC transporters, inositol	
RT	phosphatases and human expressed sequence tags.";	
RL	Yeast 13:583-589(1997).	
CC	-1- FUNCTION: GENETICALLY INTERACTS WITH CIN8.	
CC	-----	
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CC	-----	
DR	EMBL; U36382; AAA79781.1; -	
DR	EMBL; U54799; AAB00196.1; -	
DR	EMBL; Z74818; CAA99086.1; -	
DR	SGD; L0002975; DEC1.	
DR	SEQUENCE 796 AA; 92808 MW; C50D7B42 CRC32;	
SO	SEQUENCE	
Query Match	6.0%;	Score 105; DB 1; Length 796;
Best Local Similarity	22.4%;	Pred. No. 2,56e-01;
Matches	19; Conservative	24; Mismatches 36; Indels 6; Gaps 6;
Db	46 KFKOSPGK-FYUNKLEBPYGLKGTITGDRISLEFL-HNPFVELGK-YDEALHYERGN 102	
Yy	128 KYRSTTVVEFEGKKLL-SFDVOTNKKRVYAOELDYLRHYLVKKKLYEFNNSPYETGY 186	
Db	103 KFKPSYELSYHWF-NKALEDSNYNQ 126	
Yy	187 IKFIENENSF-WYDMPAPAGDKFDQ 210	
RESULT	12	
ID	YME4_YEAST	STANDARD;
AC	004711;	PRT;
DT	01-NOV-1997 (Rel. 35, Created)	1320 AA.
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-DEC-1999 (Rel. 39, Last annotation update)	
DE	TRANSPOSON T41 PROTEIN B.	
GN	TY1B OR YML044W OR YM9827.08.	
OS	Saccharomyces cerevisiae (Baker's yeast).	
OC	Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;	
CC	Saccharomycetaceae; Saccharomyces.	
RN	[1]	
RP	SEQUENCE FROM N.A.	

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RC STRAIN-S288C / AB972;
RA ODELL C., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
CC -----
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CC -----
DR EMBL: Z47816; GAB87830.1; -
DR PROSITE: PS00141; ASP_PROTEASE; 1.
KW Transposable element; Hypothetical protein; Hydrolase;
KM Aspartyl protease; ATP-binding.
FT ACT SITE 34 34
FT NP BIND 1204 1211
FT SEQUENCE 1328 AA; 150945 MW; 17EA7E22 CRC32;
SQ
Query Match 6.0%; Score 106; DB 1; Length 1328;
Best Local Similarity 28.6%; Pred. No. 1,92e+01;
Matches 20; Conservative 23; Mismatches 25; Indels 2; Gaps 2;

Db 1009 LMANKKITTLTKKQYDTRINIGESDNEIQDYIL-GLEIKYRGKYMKLGMSNLSITE-KI 1066
1 1111 : : : : : : : : : : : : : : : : : : : : : : : : :
168 IVRNKRLVEFNNSPPEGYIKFEIENESFMYDMAPGDPKPSKYLMMYNDKMVKSD 227
228 VKIEVYLTTR 237

Db 1067 PKLANPLNPK 1076
1 1 1 1 1 1 1
228 VKIEVYLTTR 237

RESULT 13
ID YMD9_YEAST STANDARD: PRT; 1328 AA.
AC 003434;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE TRANSPONSON TY1 PROTEIN B.
DE TY1B OR YML039W OR YM8054.04.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA CONNOR R., CHURCHER C., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
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CC -----
DR EMBL: Z48430; GAB89330.1; -
DR PROSITE: PS00141; ASP_PROTEASE; 1.
KW Transposable element; Hypothetical protein; Hydrolase;
KM Aspartyl protease; ATP-binding.
FT ACT SITE 34 34
FT NP BIND 1204 1211
FT SEQUENCE 1328 AA; 151036 MW; F4A24298 CRC32;
SQ
Query Match 6.0%; Score 106; DB 1; Length 1328;
Best Local Similarity 28.6%; Pred. No. 1,92e+01;
Matches 20; Conservative 23; Mismatches 25; Indels 2; Gaps 2;

Db 1009 LMANKKITTLTKKQYDTRINIGESDNEIQDYIL-GLEIKYRGKYMKLGMSNLSITE-KI 1066

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[illegible]

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RL Nucleic Acids Res. 14:3475-3485(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041864.
RA WARMINGTON J.R., MARING R.B., NEWLON C.S., INDGE K.J., OLIVER S.G.;
RT "Nucleotide sequence characterization of Ty 1-17, a class II
RL Nucleic Acids Res. 13:6679-6693(1985).
RN [3]
RP SEQUENCE FROM N.A.
RA OLIVER S.G., ANWAR R., BROWN A., GENT M.E., INDGE K.J., JAMES C.M.,
RA STATEVA L.I.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
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CC -----
DR EMBL: X03840; CAA27458.1; -
DR EMBL: X59720; E264443; -
DR PIR: B23496; B23496.
DR PIR: S19345; S19345.
KW Transposable element; Hypothetical protein; Hydrolase;
KW Aspartyl protease; ATP-binding.
FT NP_BIND 1223 1230 ATP (POTENTIAL).
SQ SEQUENCE 1347 AA; 154069 MW; 71FC7229 CRC32;

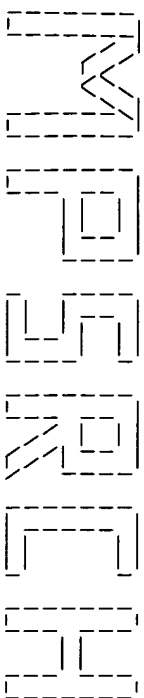
Query Match 6.0%; Score 105; DB 1; Length 1347;
Best Local Similarity 29.2%; Pred. NO. 2.56e-01;
Matches 21; Conservative 23; Mismatches 26; Indels 2; Gaps 2;

Db 1028 LNANKKITTAKKQYDFKIILGESDNEIOYDIL-GLEIKYQRSYMKLGMEKSLTE-KL 1085
QY 168 LVKNNKKLYEENNSPYETGYIKFIENENSEFWYDMMPAGDKRFDQSKYLLMNYNDNKKMYDSKD 227
Db 1086 PKLNVPILNPKGK 1097
QY 228 VKIEVYLTTKKK 239

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Search completed: Thu Apr 20 15:09:35 2000
 Job time : 88 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 20 15:13:54 2000; Maspar time 17.90 Seconds
Tabular output not generated. 629.702 Million cell updates/sec

Title: >US-09-150-947-12
Description: (1-239) from US09150947.pep
Perfect Score: 1763
Sequence: 1 ESQPDKPKDELHKSKFTGL.....NKMVDSKDVKIEVYLTTRKK 239

Scoring table:
PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r62
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 46.393; Variance 108.813; scale 0.426

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1760	99.8	266	1	ENSAB6 enterotoxin B precurs	2.96e-284
2	1183	67.1	266	1	ENSAC1 enterotoxin C-1 precu	1.19e-180
3	1156	65.6	266	2	S11885 enterotoxin C3 - Stap	7.73e-176
4	1148	65.1	266	2	A60114 enterotoxin C-2 precu	2.05e-174
5	746	42.3	251	1	S29659 exotoxin type A precu	1.75e-103
6	704	39.9	236	2	S18789 exotoxin A precursor	3.53e-96
7	694	39.4	236	2	S18783 exotoxin type A precu	1.92e-94
8	690	39.1	236	2	S18786 exotoxin type A precu	9.49e-94
9	598	33.9	250	1	A26152 streptococcal pyrogen	7.07e-78
10	412	23.4	258	2	A31953 enterotoxin D precurs	1.85e-46
11	375	21.3	257	2	A28664 enterotoxin A precurs	2.27e-40
12	373	21.2	253	2	A29566 enterotoxin A - Staph	4.82e-40
13	329	18.7	257	2	A28179 enterotoxin E precurs	6.51e-33
14	165	9.4	235	2	A30509 exotoxin C precursor	4.19e-08
15	117	6.6	509	2	D69832 probable Rheske [2Fe-	5.91e-02
16	117	6.6	592	2	C70108 peptidase homolog - L	1.32e-01
17	114	6.5	689	1	E70408 ferritin iron transpor	2.25e-01
18	112	6.4	208	2	S72286 ribosomal protein S4	2.25e-01
19	112	6.4	517	2	S22974 cytochrome P450 52A8	1.73e-01
20	113	6.4	1749	2	S69972 Tyb protein - yeast	3.80e-01
21	110	6.2	411	2	C70343 conserved hypothetical	3.80e-01
22	110	6.2	433	2	T14282 embryonic callus pr	3.80e-01
23	108	6.1	225	2	C70422 hypothetical protein	6.39e-01

24	108	6.1	226	2	F64507 hypothetical protein	6.39e-01
25	105	6.0	868	2	T02635 D2 protein homolog -	1.38e+00
26	106	6.0	1328	2	S50948 Tyb protein - yeast	1.07e+00
27	106	6.0	1328	2	S52481 Tyb protein - yeast	1.07e+00
28	105	6.0	1328	2	B28097 Tyb protein - yeast	1.38e+00
29	106	6.0	1755	2	S69963 Tyb protein - yeast	1.07e+00
30	106	6.0	1755	2	S69960 Tyb protein - yeast	1.07e+00
31	106	6.0	1755	2	S69979 Tyb protein - yeast	1.07e+00
32	106	6.0	1755	2	S69866 Tyb protein - yeast	1.07e+00
33	106	6.0	1755	2	S69839 Tyb protein - yeast	1.07e+00
34	106	6.0	1755	2	S69980 Tyb protein - yeast	1.07e+00
35	106	6.0	1755	2	S50663 Tyb protein - yeast	1.07e+00
36	106	6.0	1755	2	S69955 Tyb protein - yeast	1.07e+00
37	106	6.0	1755	2	S70298 Tyb protein - yeast	1.07e+00
38	106	6.0	1755	2	S50641 Tyb protein YER138c	1.07e+00
39	106	6.0	1755	2	S69975 Tyb protein - yeast	1.07e+00
40	106	6.0	1755	2	S69982 Tyb protein - yeast	1.07e+00
41	106	6.0	1755	2	S57045 Tyb protein - yeast	1.07e+00
42	105	6.0	1755	2	S69957 Tyb protein - yeast	1.38e+00
43	106	6.0	1756	2	S69983 Tyb protein - yeast	1.07e+00
44	106	6.0	1793	2	S52601 Tyb protein - yeast	1.07e+00
45	106	6.0	1810	2	S69973 Tyb protein - yeast	1.07e+00

ALIGNMENTS

RESULT	ENTRY	TITLE	ORGANISM	DATE
1	ENSAB6	#type complete enterotoxin B precursor -	Staphylococcus aureus	
		#formal name Staphylococcus aureus		
		24-Apr-1984 #sequence revision 15-Oct-1996 #text change		
		18-Jun-1999		
ACCESSIONS	S27360; A92065; S27240; A01815			
REFERENCE	S27360			
#authors	Jones, C.L.; Khan, S.A.			
#journal	J. Bacteriol. (1986) 166:29-33			
#title	Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.			
#cross-references	MUID:86168029			
#accession	S27360			
#molecule_type	DNA			
#residues	1-266	#label JON		
#cross-references	EMBL:M1118; NID:g152999; PIDN:AAA8550.1;			
#accession	PID:g153000			
#experimental_source	strain S6			
REFERENCE	A92065			
#authors	Huang, I.Y.; Bergdoll, M.S.			
#journal	J. Biol. Chem. (1970) 245:3511-3517			
#title	The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.			
#cross-references	MUID:71007902			
#accession	A92065			
#molecule_type	protein			
#residues	28-55, 'NND', '59-68', 'NE', '71', 'FDLIV', '78-117', '119-127', 'N', '129', 'D', '131-132', 'ENT', '136-148', 'GN', '151-156', 'Y', '157-184', 'EQ', '187-232', 'N', '234-245', 'ND', '248-266			
#label	HVA			
#experimental_source	strain S-6			
REFERENCE	A92064			
#authors	Huang, I.Y.; Bergdoll, M.S.			
#journal	J. Biol. Chem. (1970) 245:3511-3517			
#title	The primary structure of staphylococcal enterotoxin B. II. Isolation, composition, and sequence of chymotryptic peptides.			
#cross-references	MUID:71007901			
#contents	annotation; chymotryptic peptides			
REFERENCE	A92063			
#authors	Huang, I.Y.; Bergdoll, M.S.			
#journal	J. Biol. Chem. (1970) 245:3493-3510			
#title	The primary structure of staphylococcal enterotoxin B. I. Isolation, composition, and sequence of tryptic peptides from oxidized entero-toxin B.			

REFERENCE	#journal	#title	#cross-references	#contents	#authors
#cross-references	MUID:71007900				
#contents	annotation; tryptic peptides				
REFERENCE	A03548				
#authors	Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunne, D.A.; Bergdoll, M.S.				
#journal	Biochemistry (1965) 4:1011-1016				
#title	Purification of staphylococcal enterotoxin B.				
#cross-references	MUID:66035792				
#contents	annotation; biological source of protein				
REFERENCE	S27240				
#authors	Alakhov, V.Y.; Klinsky, E.Y.; Kolesov, M.I.; Maurer-Fogy, I.; Moskalova, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.; Shemchukova, O.B.; Severin, E.S.				
#journal	Eur. J. Biochem. (1992) 209:823-828				
#title	Identification of functionally active fragments of staphylococcal enterotoxin B.				
#cross-references	MUID:93049338				
#accession	S27240				
#molecule-type	protein				
#residues	28-42;128-148 #label ALA				
CLASSIFICATION	superfamily enterotoxin B				
KEYWORDS	enterotoxin; extracellular protein; toxin				
FEATURE					
1-27	#domain signal sequence #status predicted #label SIG\				
28-266	#product enterotoxin B #status experimental #label MAT\				
120-140	#disulfide_bonds #status experimental #label MAT\				
SUMMARY	#length 266 #molecular_weight 31436 #checksum 4249				
Query Match	99.8%; Score 1760; DB 1; Length 266;				
Best Local Similarity	99.6%; Pred. No. 2,96e-284;				
Matches	238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
Db	28 ESQPPKPELHKKSKFTGLMKNKLYDDNHVSAINVKSIDQFLYFDLIYSIKTRIGN 87				
Qy	1 ESQPPKPELHKKSKFTGLMKNKLYDDNHVSAINVKSIDQFLYFDLIYSIKTRIGN 60				
Db	88 YNNVRYEFNNKLDADKKRYVDYFQANYYOCYFSSKRTDINSQTDKRTCYGAT 147				
Qy	61 YNNVRYEFNNKLDADKKRYVDYFQANYYOCYFSSKRTDINSQTDKRTCYGAT 120				
Db	148 HNGNQLDKRSTVRYFEDGKNLSEFDVQNKKKYAOELDYLRHLYVNNKKLYEENNS 207				
Qy	121 HNGNQLDKRSTVRYFEDGKNLSEFDVQNKKKYAOELDYLRHLYVNNKKLYEENNS 180				
Db	208 PYETGYIKFIEENSEFWYDMPAPGDKFDQSKYILMYNDKMYDSKDYKIEVYLTTRKK 266				
Qy	181 PYETGYIKFIEENSEFWYDMPAPGDKFDQSKYILMYNDKMYDSKDYKIEVYLTTRKK 239				
RESULT	2				
ENTRY	ENSAC1 #type complete				
TITLE	enterotoxin C-1 precursor - Staphylococcus aureus				
ORGANISM	#formal_name Staphylococcus aureus				
DATE	15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999				
ACCESSIONS	S06356; A01816				
REFERENCE	S06356				
#authors	Bohach, G.A.; Schlievert, P.M.				
#journal	Mol. Gen. Genet. (1987) 209:15-20				
#title	Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to other pyrogenic toxins.				
#cross-references	MUID:88038352				
#accession	S06356				
#molecule-type	DNA				
#residues	1-266 #label BOH				
REFERENCE	A01816				
#authors	Schmidt, J.J.; Spero, L.				
#journal	J. Biol. Chem. (1983) 258:6300-6306				
#title	The complete amino acid sequence of staphylococcal enterotoxin C-1.				
#cross-references	MUID:83213327				
#accession	A01816				

GENETICS	##molecule_type	protein	##residues	28-75,'IL',78-176,'N',178-266	##label	SCH
CLASSIFICATION	gene	entC1	##superfamily	enterotoxin B		
KEYWORDS	FEATURE	1-27	enterotoxin			
28-266						
120-137						
SUMMARY	length 266	##molecular_weight	30546	##checksum	4489	
Query Match	67.1%	Score	1183;	DB 1;	Length	266;
Best Local Similarity	66.8%;	Pred. No.	1.19e-180;			
Matches	161;	Conservative	40;	Mismatches	34;	Indels 6; Gaps 6;
Db	ESQDPPTDELHKASKFPGMLNKKVLYLDHIVYATKVSVDKRLADLIYNTSDKKLN	87				
Qy	1 ESQDPKPEDELHKSSKFGMLNKKVLYLDHNVSAINKSLDQFLYDLYISIKDKRLGN	60				
Db	YDKVTELLNGLAKKRYKDEVDVYGSNYVNCYFSSK-DNV-GKLVGG-KTCMYGGITK	144				
Qy	61 YDNVAVEKKNLDADKYDKYDVFPGANYYYQCFSKKTNDINSHEDKKRTCMYGVTE	120				
Db	145 HEGNHFDGNLQNVLYRVYENKRRNTISFVOTDKRSVTAOELDIKARNFLINKNLYEFN	204				
Qy	121 HNGNOLDK-Y-RSLTVRFVEEDGKMLSDVQTNKKRYTAOELDYLTFRHYLVKNNKLYEFN	178				
Db	205 SSPVETGKIRKLENNGNFEMYDMPADQDKDQSKYLYMNTKNTVSKSGVKTIEVHLTK	264				
Qy	179 NSPTGTGKIFLEND-NSFWYDMPADQDKDQSKYLYMNTKNTVSKSGVKTIEVHLTK	237				
Db	265 N 265					
Qy	238 K 238					
RESULT	3					
ENTRY	511885	##type	complete			
TITLE	enterotoxin C3 - Staphylococcus aureus					
ORGANISM	19-Mar-1997	##formal_name	Staphylococcus aureus			
DATE	16-Jul-1999	##sequence_revision	19-Mar-1997	##text_change		
ACCESSION	511885					
REFERENCE	511885					
##authors	Howe, C.J.; Hackett, S.P.; Bohach, G.A.					
##journal	Mol. Gen. Genet. (1990) 220:329-333					
##title	Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of all three type C staphylococcal enterotoxins.					
##cross-references	MUID:90220508					
##accession	511885					
##status	preliminary					
##molecule_type	DNA					
##residues	1-266	##label	HOV			
##cross-references	GB:X51661; NID:946570; PIDN:CAA35972.1; PID:946571					
CLASSIFICATION	##superfamily	enterotoxin B				
SUMMARY	length 266	##molecular_weight	30671	##checksum	6135	
Query Match	65.6%;	Score	1156;	DB 2;	Length	266;
Best Local Similarity	66.0%;	Pred. No.	7.73e-176;			
Matches	159;	Conservative	40;	Mismatches	36;	Indels 6; Gaps 6;
Db	ESQDPDPMDDIHKSEFPGTGMNKKVLYDDHIVYATKVSVDKRLADLIYNTSDKKLN	87				
Qy	1 ESQDPKPEDELHKSSKFGMLNKKVLYLDHNVSAINKSLDQFLYDLYISIKDKRLGN	60				
Db	YDKVTELLNGLAKKRYKDEVDVYGSNYVNCYFSSK-DNV-GKLVGG-KTCMYGGITK	144				
Qy	61 YDNVAVEKKNLDADKYDKYDVFPGANYYYQCFSKKTNDINSHEDKKRTCMYGVTE	120				
Db	145 HEGNHFDGNLQNVLYRVYENKRRNTISFVOTDKRSVTAOELDIKARNFLINKNLYEFN	204				

121 HNGNLDK-Y-RSITVRFEEDGKNLSDVQTNKKYTAQELDYTRHYLVKNNKLYEFN 178
QY 205 SSPEYTGIFKFIENNGNTFWYDMPAPGDKFQDSKYLMMYNDNKTVDKSVKIEVHLTK 264
QY 179 NSPYETGIFKFIENE-NSFWYDMPAPGDKFQDSKYLMMYNDNKNVDSKDYKIEVYLTTK 237
Db 265 N 265
QY 238 K 238

RESULT 4
ENTRY
TITLE A60114 #type complete
ALTERNATE_NAMES enterotoxin C-2 precursor - Staphylococcus aureus
ORGANISM enterotoxin C-3 precursor
#formal_name Staphylococcus aureus
DATE 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
ACCESSIONS A60114; B60114; A33866
REFERENCE A60114
#authors Bohach, G.A.; Schlievert, P.M.
#journal Infect. Immun. (1989) 57:2249-2252
#title Conservation of the biologically active portions of staphylococcal enterotoxins C1 and C2.
#cross-references MUID:89277549
#accession A60114
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-266 ##label BOH
#accession B60114
#molecule_type protein
#residues 28-66 ##label BOH2

REFERENCE A33866
#authors Couch, J.L.; Betley, M.J.
#journal J. Bacteriol. (1989) 171:4507-4510
#title Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests that intergenic recombination causes antigenic variation.
#cross-references MUID:89327174
#accession A33866
#status preliminary
#molecule_type DNA
#residues 1-266 ##label COU
#cross-references GB:M28364; NID:9153003; PIDN:AAA26624.1; PID:9153004

GENETICS
#gene entC2
CLASSIFICATION #superfamily enterotoxin B
FEATURE 1-27
1-27 #domain signal sequence #status predicted #label SIG
28-266 #product enterotoxin C-2 #status predicted #label MAT
SUMMARY #length 266 #molecular_weight 30604 #checksum 5494

Query Match 65.1%; Score 1148; DB 2; Length 266;
Best Local Similarity 65.6%; Pred. No. 2,05e-174;
Matches 18; Conservative 40; Mismatches 37; Indels 6; Gaps 6;

Db 28 ESQPPPTDELLHKSSEFTGMNMYLYDXDHYVSATKYMSVDKFLAHLIYNISDKILN 87
QY 1 ESQPPKPELDLHKSSTFGMLNMYLYDXDHYVSATKYMSVDKFLAHLIYNISDKILN 60
Db 88 YDKYKTELLNEDLAKKYDEVVDVYGSNYVYVYCFSSK-DNV-KGVYGG-KTCMYGGITK 144
QY 61 YDNVVEFKNNKLDKYYDKDYVDVYGVANYVYQCYFSKKTNDINSHETDKRKTMYGVYTE 120
Db 145 HEGNFDGNGNONTVIRYENKKNRTISFENQTDKSVTAQELDIARFNLNKKLYEFPN 204
QY 121 HNGNLDK-Y-RSITVRFEEDGKNLSDVQTNKKYTAQELDYTRHYLVKNNKLYEFPN 178
Db 205 SSPEYTGIFKFIENNGNTFWYDMPAPGDKFQDSKYLMMYNDNKTVDKSVKIEVHLTK 264
QY 179 NSPYETGIFKFIENE-NSFWYDMPAPGDKFQDSKYLMMYNDNKNVDSKDYKIEVYLTTK 237

Db 265 N 265
QY 238 K 238

RESULT 5
ENTRY
TITLE S29659 #type complete
ALTERNATE_NAMES erythrogenic toxin: scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phase T12
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
ACCESSIONS S29659; S18782; S18784; S18785; S18791; S18796; S18797;
S18800
REFERENCE S29659
#authors Weeks, C.R.; Ferretti, J.J.
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#cross-references MUID:86166804
#accession S29659
#molecule_type DNA
#residues 1-251 ##label WFE
#cross-references GB:U04053; EMBL:M19350; NID:91877426; PIDN:AAC48868.1; PID:91877430

REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession S18782
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEL
#cross-references EMBL:X61560; NID:947287; PIDN:CAA43758.1; PID:947288
#experimental_source Streptococcus pyogenes strain MGA5165 isolate Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18784
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEA
#cross-references EMBL:X61556; NID:947291; PIDN:CAA43754.1; PID:947292
#experimental_source Streptococcus pyogenes strain MGA5167 isolate Minnesota unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18785
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEZ
#cross-references EMBL:X61559; NID:947293; PIDN:CAA43757.1; PID:947294
#experimental_source Streptococcus pyogenes strain MGA5167 isolate Texas unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18791
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEY
#cross-references EMBL:X61555; NID:947309; PIDN:CAA43753.1; PID:947310
#experimental_source Streptococcus pyogenes strain MGA5327 isolate Arizona unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18796
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA

```

#residues      9-244 ##label NEO
##cross-references EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320
#experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note          the nucleotide sequence was submitted to the EMBL Data
               Library, September 1991
#accession     S18797
##status       nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues     9-244 ##label NEH
##cross-references EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
#experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note          France unassigned phage
               the nucleotide sequence was submitted to the EMBL Data
               Library, September 1991
#accession     S18800
##status       nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues     9-228 ##label NES
##cross-references EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328
#experimental_source Streptococcus pyogenes strain MGAS500 isolate New
               Zealand unassigned phage
               the nucleotide sequence was submitted to the EMBL Data
               Library, September 1991
GENETICS
#gene          speA; speAI
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS       exotoxin
FEATURE        1-30   #domain signal sequence
                31-251 #product exotoxin type A #status predicted #label SIG\
SUMMARY        #length 251 #molecular-weight 29246 #checksum 1475
Query Match    42.3%; Score 746; DB 1; Length 251;
Best Local Similarity 50.2%; Pred. No. 1.75e-103;
Matches 119; Conservative 43; Mismatches 59; Indels 16; Gaps 9;
Db 30 AQQDDPSQLHRSSLVKNL-QNITFLYEGDPYTHENKVSQDLISHDLIYNVSGP---NY 85
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 2 SQPPKPDELHKSSKFTEGLMKMVKVLVDNDHNVAINKSIDOFLYEDLISIKDTKLGNV 61
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 86 DKLRTELKNOMATLEKDNVDIVGEVYLHCYC-----E-NA-E--RSACIYGVTNH 136
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 62 DNVRKEFNKKDLADKKDYDVFGANTYYQCYSFKKTINDINSHEIDKRKTCMTGVTEN 121
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 137 EGNHLIELPKKIIVKVSIDQSLSFDIEIENKKNVTAQELDLYKKRYLLTDKQOLYNGPSK 196
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy 122 NGNQDLDKYRSTIVAFVEDEGKNILSFDVQTNNKKVTAQELDLYLRPHLYLVKKKKILEFNPNSP 181
   ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 197 YETGIYKIPKSKSEFPDFEPPE-E-FTOSKIYIMTKDNDETLDSTNTSQLEYLTTR 251
   |||||||||::||::||::||::||::||::||::||::||::||::||::||
Qy 182 YETGIKIKI-ENENSFWYDMWPAFGDKFDQSKYLMYMDNRKMVDSKDVKRIEYVLTTR 237
   |||||||||::||::||::||::||::||::||::||::||::||::||::||
RESULT 6
ENTRY      S18789           #type fragment
TITLE      exotoxin A precursor (allele 4) - Streptococcus pyogenes
            (strain PGAS262 isolate California) (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM   #formal name Streptococcus pyogenes
            strain MGAS262 isolate California
DATE       29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
            16-Jul-1999
ACCESSIONS S18789
REFERENCE   S18782
AUTHORS     Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
JOURNAL     J. Exp. Med. (1991) 174:1271-1274
TITLE       Characterization and clonal distribution of four alleles of
            the spa gene encoding pyrogenic exotoxin A (scarlet fever
            toxin) in Streptococcus pyogenes.
#cross-references MIMD:92044323
#accession   S18789
#status      nucleic acid sequence not shown; translation not shown

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##molecule_type DNA
##residues 1-236 ##label NEL
##cross-references EMBL:X61573; NID:g47303; PIDN:CAA43771.1; PID:g47304
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991

GENETICS
#gene speA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
FEATURE 1-22
23-236 #domain signal sequence (fragment) #status predicted
#product exotoxin A (fragment) #status predicted #label
MAT

SUMMARY #length 236 #checksum 3493

Query Match 39.9%; Score 704; DB 2; Length 236;
Best Local Similarity 46.5%; Pred. No.3,53e-96;
Matches 107; Conservative 53; Mismatches 54; Indels 16; Gaps 8;

Db 22 AQDDPNFSQLHRSSLVKNL-QNTFLYEGDPVYHVNKSVDDLSHLLIYNVG--L-NY 77
:::|||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 2 SQDPRKDEHLKSSSKFGLMENKKVLYDDNHSAIVKSIDQFLYFLDIYSIKDKLCNY 61
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 78 DKLTALKNNEMSTLFENKAVNDLYGEVEYYHYCYLCR-----NA-----KRRACTGGVTNH 128
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 62 DNVAVEREKMDLADKKYKDXYDGANVYOCYCFSSKTKNDINSHETDRKTCMGCVTEH 121
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 129 EGNLELPKNILVKVSIIDGIOSPLFIETSKKWATVQNQELDYVRKHLDINKOLYTNGPSK 188
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 122 NGNOLDKRTSYTRVPEDGKNLLSPVOYRNKKRVTRQDELDTLTRIYLAKNKRIEFNNSP 181
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 189 YETGYIKFKRETKEFWDFEPP-E-FNQVYLMILYKNDETLDSSTSQI 236
|||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 182 YETGYIKFIENEN-SFYWDMPAPAGDGKFOGSKYLMMYNDNMKVDSKDVKI 230
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
ENTRY S18783 #type fragment
TITLE exotoxin type A precursor (allele 3) - Streptococcus pyogenes
phase (strain MGAS158 isolate Nebraska and others)
(fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM #formal_name Streptococcus pyogenes phase
#variety strugin MGAS158 isolate Nebraska; strain MGAS485 isolate
yugoslavia; strain MGAS491 isolate United Kingdom; strain
MGAS624 isolate Germany; strain MGAS495 isolate Germany
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
16-Jul-1999
DATE S18783; S18793; S18794; S18801; S18798
S18783; S18782
REFERENCES Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.,
J. Exp. Med. (1991) 174:1271-1274
#authors Characterization and clonal distribution of four alleles of
#journal the speA gene encoding pyrogenic exotoxin A (scarlet fever
#title toxin) in Streptococcus pyogenes.
#cross-references M0ID:92044323
#accession S18783
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEL
##cross-references EMBL:X61566; NID:g47289; PIDN:CAA43766.1; PID:g47290
##experimental_source strain MGAS158 isolate Nebraska unassigned phase
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
#accession S18793
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-236 ##label NEA
##cross-references EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
##experimental_source strain MGAS485 isolate yugoslavia unassigned phase
##note the nucleotide sequence was submitted to the EMBL data
Library, September 1991
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	#accession	S18794	#status	nucleic acid sequence not shown; translation not shown
	##molecule_type	DNA	##residues	1-236 ##label NEZ
	##cross-references	EMBL:X61570; NID:g47315; PIDN:CAA43768.1; PID:g47316	##experimental_source	strain MGAS491 isolate United Kingdom unassigned phage
	##note	the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
	#accession	S18801	#status	nucleic acid sequence not shown; translation not shown
	##molecule_type	DNA	##residues	1-236 ##label NEY
	##cross-references	EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334	##experimental_source	strain MGAS624 isolate Germany unassigned phage
	##note	the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
	#accession	S18798	#status	nucleic acid sequence not shown; translation not shown
	##molecule_type	DNA	##residues	1-236 ##label NEO
	##cross-references	EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324	##experimental_source	strain MGAS495 isolate Germany unassigned phage
	##note	the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
	GENETICS			
	#gene	speA3	CLASSIFICATION	#superfamily enterotoxin B
	KEYWORDS	exotoxin		
	FEATURE			
	1-22	##domain signal sequence (fragment) #status predicted		
		#label SIG\		
	23-236	##product exotoxin type A (fragment) #status predicted		
		#label MAT		
	SUMMARY	#length 236 #checksum 612		
	Query Match	39.4%; Score 694; DB 2; Length 236;		
	Best Local Similarity	48.3%; Pred. No. 1,92e-94;		
	Matches	111; Conservative 44; Mismatches 59; Indels 16; Gaps 9;		
	Db	22 AACDDPDSOLHRSSLYVNL-QNTIFYEGDPVYHEWKSVDQLSHDLTYNSGP---NY 77		
	Oy	2 SQPPKFDLEHKSKSPFGLENKKVLYLDNNHSAIWNKSIDQFLFYSLTKDKRLGNY 61		
	Db	78 DKLTELKNQEMATLFPKKNIDIVGYEYHYLCYLCA---E-NA-E--RSACIYGVTNH 128		
	Oy	62 DNVAVEREKNDLADKYDKAYDVDFGANYYQCCEFSKKTNDINSHEDRKRTCMGCVTEH 121		
	Db	129 EGNHLETPKRIIVAVSIDIQSISFPIETNKKAWTVAOELDYKRYKLTLDNKOLYTNGPSK 188		
	Oy	122 NGNOLDYRSTLYTVAPEVDGKNLLSFVDQTAKKKVTAQOELDLYLTRHLVYNKRKLTFENNSP 181		
	Db	189 YETGIKFIPKNESEPFDEFPPEP-E-FIOSKTLMIYKDNENTLDSITSI 236		
	Oy	182 YETGIKFI-ENSENSEWYDMPAPAGDFQDSKYLMIYNDKNVDSKDVKI 230		
	RESULT	8		
	ENTRY	S18786	#type fragment	
	TITLE	exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate California and others)		
	ALTERNATE_NAMES	(fragment)		
	ORGANISM	#formal name Streptococcus pyogenes phage scarlet fever toxin		
	#variety	strain MGAS250 isolate California; strain MGAS251 isolate California; strain MGAS256 isolate California; strain MGAS285 isolate Colorado; strain MGAS480 isolate Yugoslavia; strain MGAS492 isolate United Kingdom; strain MGAS496 isolate Germany		
	DATE	29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999		
	ACCSSIONS	S18786; S18787; S18788; S18790; S18792; S18795; S18799		
	REFERENCE	S18782		

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#authors      Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal      J. Exp. Med. (1991) 174:1271-1274
#title        Characterization and clonal distribution of four alleles of
              the spa gene encoding pyrogenic exotoxin A (scarlet fever
              toxin) in Streptococcus pyogenes.
#cross-references MIM:92044323
#accession   S18786
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:947297; PIDN:CAA43759.1; PID:947298
##experimental_source strain MGA5250 isolate California unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18787
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:947299; PIDN:CAA43760.1; PID:947300
##experimental_source strain MGA5251 isolate California unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18788
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:947301; PIDN:CAA43761.1; PID:947302
##experimental_source strain MGA5256 isolate California unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18790
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:947305; PIDN:CAA43762.1; PID:947306
##experimental_source strain MGA5285 isolate Colorado unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18792
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:947311; PIDN:CAA43763.1; PID:947312
##experimental_source strain MGA5480 isolate Yugoslavia unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18795
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:947317; PIDN:CAA43764.1; PID:947318
##experimental_source strain MGA5492 isolate United Kingdom unassigned
              phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18799
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:947325; PIDN:CAA43765.1; PID:947326
##experimental_source strain MGA5496 isolate Germany unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
GENETICS
#gene         spa2
CLASSIFICATION
#superfamily enterotoxin B
KEYWORDS      exotoxin
FEATURE
1-22
23-236
#domain signal sequence (fragment) #status predicted
#label STG\
#product exotoxin type A (fragment) #status predicted
#label MAT
#length 236 #checksum 1685
SUMMARY

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Gaps				9
Db	22	A00DDPDSOLHRSLSLVKNTL-QNTIPLYEGDPVTHENKVSVDOLSHDLIYNVSGP--NY 77		
Qy	2	SPDDPPEDELHRSKSKFTGLMENNKKVLYLDNDHVSAINVKSIDQFLPYDLIYSIKPTKLGNY 61		
Db	78	DLKLTLELKNQEMATLPRKDKVNDIYSEVYHLCYC---E-NA-E---RSACITGGVYTNH 128		
Qy	62	DIVRVEFEKKNDLADKKDKVDVFGANYYYQCYFSKKTNDINSHECTKRKTCMGGVTEH 121		
Db	129	EGNHLEIPKKIYKVSIDGQSLSFDIETKKNMATAELDYKVKRYLTNDNKOLTYNPGSK 188		
Qy	122	NGNDLKYRSITYRYVEDGKNLLSPDVQTKKKVTAQELDYLTRHYLYKNNKKIIEFNNSP 181		
Db	189	YETGYIKFIPKNKESFWDFEPEP-E-FTQSKYLMYIKDNETIDSNTSQI 236		
Qy	182	YETGYIKFI-ENENSEFWYDMAPAGDKFDQSKYLMYNDNMKMDSKDVKI 230		
.RESULT	9			
ENTRY	A26152	#type complete		
TITLE	streptococcal pyrogenic exotoxin type A precursor -			
ALTERNATE_NAMES	scarlet fever toxin; SPE type A (spea)			
.ORGANISM	#formal.name Streptococcus sp.			
DATE	10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999			
ACCESSIONS	A26152			
REFERENCE	A26152			
#authors	Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.			
#journal	Mol. Gen. Genet. (1986) 203:354-356			
#title	Streptococcal pyrogenic exotoxin type A (scarlet fever toxin)			
#cross-references	is related to Staphylococcus aureus enterotoxin B.			
#accession	MOID:86284313			
#molecule-type	A26152			
#residues	1-250	#label JOH		
CLASSIFICATION	#superfamily enterotoxin B			
KEYWORDS	exotoxin			
SUMMARY	#length 250 #molecular-weight 29168 #checksum 8233			
Query Match	33.9%	Score 598	DB 1	Length 250
Best Local Similarity	43.8%	Pred. No. 7,07e-78		
Matches 102	Conservative	47	Mismatches 67	Indels 17
Gaps				10
Db	34	PKPSQIORSNLVTKFKIYIFEM-RVTLVTHENKVSVDOLSHDLIYNVSGP--NYDKLK 89		
Qy	6	PRDELHRSKSKFTGLMENNKKVLYLDNDHVSAINVKSIDQFLPYDLIYSIKPTKLGNYDNR 65		
Db	90	TELKNDQEMATLPRKDKVNDIYSEVYHLCYC---E-NA-E---RSACITGGVYTNHGNH 140		
Qy	66	VEKKNNDLADKKDKVDVFGANYYYQCYFSKKTNDINSHECTKRKTCMGGVTEHNGN 125		
Db	141	LEIPKKIYKVSIDGQSLSFDIETKKNMATAELDYKVKRYLTNDNKOLTYNPGSKYETG 199		
Qy	126	LKYSRISITYRYVEDGKNLLSPDVQTKKKVTAQELDYLTRHYLYKNNKKIIEFNNSPETG 185		
Db	200	YIKFIPKNKESFWDFEPEP-E-FTQSKYLMYIKDNETIDSNTSQIEVYLYTK 250		
Qy	186	YIKFI-ENENSEFWYDMAPAGDKFDQSKYLMYNDNMKMDSKDVKIIEVYLYTK 237		
RESULT	10			
ENTRY	A33953	#type complete		
TITLE	enterotoxin D precursor - Staphylococcus aureus			
ORGANISM	#formal.name Staphylococcus aureus			
DATE	09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 26-Aug-1999			
ACCESSIONS	A33953			
REFERENCE	A33953			

#authors	J. Bacteriol.	(1989) 171:4799-4806
#journal	Genetic and molecular analyses of the gene encoding	staphylococcal enterotoxin D.
#title	#cross-references MUID:89359112	
#accession	A33953	
#status	Preliminary	
##molecule-type	DNA	
##residues	1-258 ##label	BAY
##cross-references	GB:M28521; NID:g1492109; PID:g758691	
CLASSIFICATION	#superfamily	enterotoxin B
SUMMARY	length 258	#molecular-weight 29746 #checksum 39
Query Match	23.4%; Score 412; DB 2;	Length 258;
Best Local Similarity	36.6%; Pred. No. 1,85e-46;	
Matches	87; Conservative	53; Mismatches 79; Indels 19; Gaps 13;
Db	33 KEKELHKKSELSALNNMKHSYADKNPIIGENSTDOFLQHTLTKKFFTLINPEDL	92
Oy	7 KPDELHKSSKTGL-MEMNKLYLD-NHVSAINKSIDOFLPDILYSISDTKLGNVDN	64
Db	93 LINFNSKEMAOFKSKNVDPYPIRSYNCY-G--GEI-----D-RTACTYGGVTPAEQN	142
Oy	65 RVEEFKNKDIAKYDDVAGANYYYQCFYSKKTNDINSHETDKRKYCYGVTGHNGN	124
Db	143 KLEKKKPIPLMYNQVKEVSLDKVOTDKKNYVOELDQAARYLOKDLKLTNNDTLG	202
Oy	125 QLDKRYSLTVAVFDG-KNLISFD-VQTNNKKVYAQELDLTRHYLVKNRKLEYFNPN-S	181
Db	203 KIORKIEFSDSDSKSYDLPDVKG-D-FPE-KOLRIYSNNKTLSTFHLIHDIYLK	258
Oy	182 -YEGYIKIFINENS-FWYDMMPAPGDKFDSOKLTMMYNDNMKVADSVKIVELYITLK	237
RESULT	11	
ENTRY	A28664	#type complete
TITLE	enterotoxin A precursor - Staphylococcus aureus (strain FRI337)	
ORGANISM	#format_name	Staphylococcus aureus
DATE	30-Jun-1989	#sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
ACCESSIONS	A28664	
REFERENCE	A28664	
#authors	Belley, M.J.; Mekalanos, J.J.	
#journal	J. Bacteriol.	(1988) 170:34-41
#title	Nucleotide sequence of the type A staphylococcal enterotoxin gene.	
#cross-references	MUID:88086892	
#accession	A28664	
##molecule-type	DNA	
##residues	1-257 ##label	BET
##cross-references	GB:M18970; NID:g153120; PID:g153121	
CLASSIFICATION	#experimental_source	strains FR1337
SUMMARY	#superfamily	enterotoxin B
Query Match	21.3%; Score 375; DB 2;	Length 257;
Best Local Similarity	35.0%; Pred. No. 2.27e-40;	
Matches	82; Conservative	56; Mismatches 77; Indels 19; Gaps 12;
Db	35 DLRRKSLEGTALCNKOIYYNEKAKTENKESHDOFLQHTLTFKGFETDHSWYNLDLV	94
Oy	10 ELHKSSKETGL-MEMNK-VLTDHDNHSAINWKSIDOFLPDLIYSIDTKLGNYDVAVE	67
Db	95 FDSKDIYDKYGGKVDLGAATYGQC-----AGC-T-PNK-TACMGYGVTLHDNRRL	144
Oy	68 FKNDLAKRYDKVDYVFAGANYYYQCFYSKKTNDINSHETDKRKYCYGVTGHNGQLD	127
Db	145 EEKKVIPILMLDGKONYPLETYTKNNKNYVOELDQAARYLOEKYNLYNSDVPFGKY	204
Oy	128 KYRSLTAVFEDGR-NLLSPD-VQTNNKKTYAQELDLTRHYLVKNRKLEYFNPN-ASPYE	183
Db	205 RGLIVFHSTEPSVNYDLFGAQQ-QYST-LARIYRNKNTINSNMHIIDITYLT	256

Oy	184	TGYIKF-IENENSFWYDMMPAPGDKFPQSGXYLLAMYNDRKNVDSKDVKEIVLYLT	236
RESULT	12	A29566	#type complete
ENTRY		enterotoxin A - Staphylococcus aureus	
TITLE		#formal_name Staphylococcus aureus	
ORGANISM		05-Jun-1968 #sequence_revision 05-Jun-1988 #text_change	
DATE		18-Jun-1993	
ACCESSIONS		A29566	
REFERENCE		A29566	
#authors		Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.	
#journal		J. Biol. Chem. (1987) 262:7006-7013	
#title		Complete amino acid sequence of staphyloccocal enterotoxin A	
#cross-references		MUID:87222293	
#accession		A29566	
#molecule_type		protein	
#residues		1-233 #label HUA	
GENETICS			
#gene		entA	
#map_position		6	
SUMMARY		#length 233 #molecular_weight 27079 #checksum 9580	
Query Match		21.2%; Score 373; DB 2; Length 233;	
Best Local Similarity		35.0%; Pred. No. 4,82e+40;	
Matches		82; Conservative 56; Mismatches 77; Indels 19; Gaps 12;	
Db	11	DLRKKSEGLGTALGNLKOIYYNEKATNKESHDFLOHTLIIFKFQFTDHSWYNDLVD	70
Oy	10	ELHSSKFTGL-MENMK-VLYDDNHWSAINVKSIDQFLVFEDLIYSIKDTKLGNVDNRYE	67
Db	71	PDSKDIDYKRGKRVLDIGAYYGQC-----AGC--T--PNK-TACMGGATLHDNNRLT	120
Oy	68	FKNRDLDADKYADVDFGANYYQQCFESKRITDINSHECTRKRTCMYGVTGEHNGNQID	127
Db	121	EERKVPINLMIDGKONVPLETYTNKNNTYOELDIQAARYQEERYNLNSDVEFGKWQ	180
Oy	128	KYRSITYAVFEEDGR-NILSPD-VQTNNKKTATQAEIDLIRHYLYKKAKKIYERN--NSPE	183
Db	181	RGLIVFHTSTEPSVNYDLFGAQGO-YSENT-LLRIRYDNKSINSENHHIDLYYT	232
Oy	184	TGYIKF-IENENSFWYDMMPAPGDKFPQSGXYLLAMYNDRKNVDSKDVKEIVLYLT	236
.RESULT	13	A28179	#type complete
ENTRY		enterotoxin E precursor - Staphylococcus aureus	
TITLE		#formal_name Staphylococcus aureus	
ORGANISM		30-Jun-1969 #sequence_revision 30-Jun-1989 #text_change	
DATE		26-Aug-1999	
ACCESSIONS		A28179	
REFERENCE		A28179	
#authors		Couch, J.L.; Solits, M.T.; Betley, M.J.	
#journal		J. Bacteriol. (1988) 170:2954-2960	
#title		Cloning and nucleotide sequence of the type E staphyloccocal	
		enterotoxin gene.	
#cross-references		MUID:88257005	
#accession		A28179	
#molecule_type		DNA	
#residues		1-257 ##label COU	
#cross-references		GB:M21319; NID:g153001; PID:g153002	
CLASSIFICATION		#superfamily enterotoxin B	
SUMMARY		#length 257 #molecular_weight 29358 #checksum 2562	
Query Match		18.7%; Score 329; DB 2; Length 257;	
Best Local Similarity		33.8%; Pred. No. 6.51e+33;	
Matches		79; Conservative 56; Mismatches 80; Indels 19; Gaps 13;	
Db	35	DLRKKSELQRNALSNLKQIYYNEKAITEKNKESDDGFLENTLLIFKQFFGHPIYNDLVD	94
Oy	10	ELHSSSKFT-GIMENMK-VLYDDNHWSAINVKSIDQFLVFEDLIYSIKDTKLGNVDNRYE	67

Db	95	IGSDANIKKKKKVVDLYGAYGYOC-----AGC--T--PNK-TTCAMGGVYLHNNBLT	144
Oy	68	FKNKDLADKTKYKVDVEGANYTYQCFSKSKTINDISHTDKRKCMTGGVYEHNGNDLD	127
Db	145	EEKRVPIINLWDGQOTVPIPIDKVTSKKEVTQVELDQARHLYLHGKGLYNSDFGCVQ	204
Oy	128	KYRSITVRVEDGKNL-LSPD-VQTKKKVTAQEDLYLRHLYLNKKKLYEPNN-SP-YE	183
Db	205	RGIVFHSSEGSIVSYDLFDAGQO-YPDY-LRIYRDNKNTINSENLHIDLXYLT	256
Oy	184	TGYIKFTIENENS-FWYDMAPAPGDKFDQSKYLLMYNDNKWVDSKIDVLEUYLT	236
RESULT	14		
ENTRY	A30509	#type complete	
TITLE	exotoxin C precursor - Streptococcus pyogenes		
ORGANISM	#format_name Streptococcus pyogenes		
DATE	31-Dec-1988	#sequence_revision 31-Dec-1988	#text_change
ACCESSIONS	A30509		
REFERENCE	A30509		
#authors	Goshorn, S.C.; Schlievert, P.M.		
#journal	Infect. Immun. (1988) 56:2518-2520		
#title	Nucleotide sequence of streptococcal pyrogenic exotoxin type C.		
#cross-references	MUID:88314303		
#accession	A30509		
#molecule_type	DNA		
#residues	1-235	#label GOS	
#cross-references	GB:M5514; NID:g153820; PID:g153821		
KEYWORDS	exotoxin		
SUMMARY	length 235	#molecular_weight 27560	#checksum 9383
Query Match	9.4%;	Score 165;	DB 2; Length 235;
Best Local Similarity	25.8%;	Pred. No. 4.19e-08;	
Matches	32;	Conservative 37;	Mismatches 49; Indels 6; Gaps 6;
Db	113	IVGGITPAQNNKVN-HKLGNGLFISGSQGNLNKKITLEKDIYTFQELDFKIRKLYMNY	171
Oy	114	MYGGVTEHNGQDLKRYSI-TVRVEDGKRLLSFDVQTKKKVTAQEDLYLRHLYLNK	172
Db	172	KIYD-AISPYVSGIEIGTKDGHQEDLDFDSNEG-TSDDIFAKKDKNRITNMKNFSHF	229
Oy	173	KLYEKNNSPYETGYIKFIENENSP-WYDMAPAPGDGFDQSKYLLMYNDNKWVDSKD-VKI	230
Db	230	DIYL 233	
Oy	231	EYVL 234	
RESULT	15		
ENTRY	D69832	#type complete	
TITLE	probable Rleske [2Fe-2S] iron-sulfur protein yhfW - Bacillus subtilis		
ORGANISM	#format_name Bacillus subtilis		
DATE	05-Dec-1997	#sequence_revision 05-Dec-1997	#text_change
ACCESSIONS	D69832		
REFERENCE	A69580		
#authors	Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoio, M.G.; Bessieres, P.; Bolochin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Briganello, S.C.; Bron, S.; Brouillet, S.; Buschli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Cornerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devane, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, S.; Fuma, S.; Galizzi, A.; Gallero, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guisepi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.		

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Kasahara, Y.; Klaeffer-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.;
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K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
Yoshikawa, H.; Danchin, A.
Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
#journal
#title
#cross-references PMID:98044033
#accession
D59932
#status
preliminary; nucleic acid sequence not shown;
translocation not shown
##molecule_type DNA
##residues 1-509 ##label KUN
##cross-references GB:Z59109; GB:AL009126; NID:g2633260; PID:e1183041;
PID:g2633375
##experimental_source strain 168
GENETICS
#gene ynfW
CLASSIFICATION
#superfamily Rieske [2Fe-2S] homology
KEYWORDS 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
FEATURE
453-499 #domain Rieske [2Fe-2S] homology #label RSK
463,465,481,484 #binding_site 2Fe-2S cluster (Cys, His, Cys, His)
(covalent) #status predicted
SUMMARY #length 509 #molecular-weight 57109 #checksum 4843
Query Match 6.6%; Score 117; DB 2; Length 509;
Best Local Similarity 28.9%; Pred. No. 5,91e-02;
Matches 24; Conservative 24; Mismatches 28; Indels 7; Gaps 6;
Db 40 GCATGTTAAELRK-RERFV-VLIENOVLTGTAATTAKVTRQADMDIDEIRFGLNH 97
||| : | : | : | : | : | : |||| : | : | : | :
QY 116 GGATE-HNGOQLRYRSTRITVAEEDKNLSFDVQTKKKRTAO--ELD--LTRHYLVKN 171
||||| : | : | : | : | : | : ||||| : | : | : | :
Db 98 ARLY-YEANOAIIDYIKGIIVDEH 119
::| ::| :| | :| :|
QY 172 KKLEFPNNSPYEGYIKFIENEN 194

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Search completed: Thu Apr 20 15:16:21 2000
Job time : 147 secs.

OY 179 NSPEYTGIFYKIENE-NSFWYDMMPAPGDKFDSKYLMTYNDNKMVDSKDVKEVYLTTR 237
Db 238 N 238
OY 238 K 238

RESULT 2
ID 006534 PRELIMINARY: PRT: 239 AA.
AC 006534;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria: Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13379; AAA26623.1; -.
DR HSSP: P34071; 1SE2.
DR PFAM: PF01123; Staph-Staph-toxin; 1.
DR Enterotoxin; Toxin; Superantigen.
FT NON TER 1
SO SEQUENCE 239 AA; 27517 MW; 1293E9CA CRC32;

Query Match 66.3%; Score 1169; DB 2; Length 239;
Best Local Similarity 66.8%; Pred. No. 2.24e-193;
Matches 161; Conservative 38; Mismatches 36; Indels 6; Gaps 6;

Db 1 ESOPDPDPDLHRSKFTGLMKNKLYDDHYVATKVSVDKFLADLYNISDKKLKN 60
OY 1 ESOPDPDPDLHRSKFTGLMKNKLYDDHYVATKVSVDKFLADLYNISDKKLKN 60
Db 61 YDKVKTLELNLAKKRYDEVYDYGSNYYVNCYFSSK-DNV-GKVTG-KTCMYGKITR 117
OY 61 YDNVRFVFKKDLADKKYDVFAGANYYYOCYFSKKTNDINSHEDKRTKTCMYGVT 120
Db 118 HEGNHEDNGMLQNVLYVYENKRTISFEVQTDKSVTAOELDIKARSLINKNLYEFN 177
OY 121 HNGNQLDK-Y-RSTIVVFEDEGKNLISFDVQTNKKVTAOELDYLTFRHYLVKKNKLYEFN 178
Db 178 SSPYETGYIKFIENNGTFWYDMMPAPGDKFDSKYLMTYNDNKMVDSKDVKEVYLTTR 237
OY 179 NSPEYTGIFYKIENE-NSFWYDMMPAPGDKFDSKYLMTYNDNKMVDSKDVKEVYLTTR 237
Db 238 N 238
OY 238 K 238

RESULT 3
ID 006532 PRELIMINARY: PRT: 239 AA.
AC 006532;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria: Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;

RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13375; AAA26619.1; -.
DR HSSP: P34071; 1SE2.
DR PFAM: PF01123; Staph-Staph-toxin; 1.
DR Enterotoxin; Toxin; Superantigen.
FT NON TER 1
SO SEQUENCE 239 AA; 27642 MW; 81CA4BC2 CRC32;

Query Match 65.9%; Score 1162; DB 2; Length 239;
Best Local Similarity 66.0%; Pred. No. 5.02e-192;
Matches 159; Conservative 41; Mismatches 35; Indels 6; Gaps 6;

Db 1 ESOPDPDPDLHRSSEFTGMDNKKLYDDHYVATKVSVDKFLADLYNISDKKLKN 60
OY 1 ESOPDPDPDLHRSKFTGLMKNKLYDDHYVATKVSVDKFLADLYNISDKKLKN 60
Db 61 YDKVKTLELNLAKKRYDEVYDYGSNYYVNCYFSSK-DNV-GKVTG-KTCMYGKITR 117
OY 61 YDNVRFVFKKDLADKKYDVFAGANYYYOCYFSKKTNDINSHEDKRTKTCMYGVT 120
Db 118 HEGNHEDNGMLQNVLYVYENKRTISFEVQTDKSVTAOELDIKARSLINKNLYEFN 177
OY 121 HNGNQLDK-Y-RSTIVVFEDEGKNLISFDVQTNKKVTAOELDYLTFRHYLVKKNKLYEFN 178
Db 178 SSPYETGYIKFIENNGTFWYDMMPAPGDKFDSKYLMTYNDNKMVDSKDVKEVYLTTR 237
OY 179 NSPEYTGIFYKIENE-NSFWYDMMPAPGDKFDSKYLMTYNDNKMVDSKDVKEVYLTTR 237
Db 238 N 238
OY 238 K 238

RESULT 4
ID 006531 PRELIMINARY: PRT: 239 AA.
AC 006531;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria: Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=4446;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13374; AAA26618.1; -.
DR HSSP: P34071; 1SE2.
DR PFAM: PF01123; Staph-Staph-toxin; 1.
DR Enterotoxin; Toxin; Superantigen.
FT NON TER 1
SO SEQUENCE 239 AA; 27612 MW; 52B18853 CRC32;

Query Match 65.4%; Score 1153; DB 2; Length 239;
Best Local Similarity 65.6%; Pred. No. 2.73e-190;
Matches 158; Conservative 41; Mismatches 36; Indels 6; Gaps 6;

Db	1	ESOPDPMDDLHKSSSEFTGTMGNKKYLYDDHYVATKVSVDKFLANDLYNIDSRELN	60
Oy	1	ESOPDPKDELLHKSSKTKTGLMKNKKVLYDXDNHVSAINVKSIDPOFLYFDLYISIDKVLGN	60
Db	61	YDKYKTELLNEDLAKKYYKDEVVYDYGSNYYVNCYFSSK-DNV-GKLVGG-KTCMYGGITK	117
Oy	61	YDNRYVEFKNKDLKKYKDKYDVFEGANYYYQCYFSKKTNDINSHEFDKRYTKMGVTE	120
Db	118	HEGHAFPNGNLQNLVAVYENKRNITISPEVOTDKSYTAOELDIKANFLINKNLYEEN	177
Oy	121	HNGQLODK-Y-RSTIVRFEDEGKNLLSFVDOTNKKRYTAOELDYLTBHYLVKNNKILEFN	178
Db	178	SSPYETGYIKFIEENNGNTFWYDMPAPGDGDFDQSKYLLAMYNDNKTVPYSVYKIEVHLTTK	237
Oy	179	NSPYETGYIKFIEENE-NSFWYDMPAPGDGDKRQSKYLLAMYNNDKNMVDVSKOVKIEVLYLTK	237
Db	238	N	238
Oy	238	K	238

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RESULT      5
ID          006533      PRELIMINARY;      PRT:      239 AA.
AC          006533;
DT          01-NOV-1996 (TREMBLrel. 01, Created)
DT          01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT          01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE          ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
OS          Staphylococcus aureus.
OC          Bacteria; Firmicutes; Bacillus/Clostridium group;
OC          Bacillus/Staphylococcus group; Staphylococcus.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN-MNCOPELAND;
RX          MDLINE: 94011313.
RA          MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT          "characterization of novel type C staphylococcal enterotoxins:
RT          biological and evolutionary implications.";
RL          Infect. Immun. 61:4254-4262(1993).
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC          STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC          -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC          PYROGENIC EXOTOXINS ARE ALL RELATED.
DR          EMBL: L13378; AAA26622.1; -.
DR          HSSP: P34071; 1STE.
DR          PFAM: PF01123; 1STE.
FM          Enterotoxin; Toxin; Supernatigen.
FT          NON_TER      1      1
SQ          SEQUENCE      239 AA;      27651 MW;      7A5C4047 CRC32;

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Query Match	65.28;	Score 1150;	DB 2;	Length 239;
Best Local Similarity	66.08;	Pred. No. 1.03e-189;		
Matches 150;	Conservative 39;	Mismatches 37;	Indels 6;	Gaps 6

Db	1	ESQDDPDPDELHKSSSEFGTGMGNKKLYLDHYVYSATKYSDVKRLAHLDLINISDKKLKN	60
	1		
Qy	1	ESQDDPKPEDELHKSSKFLGMLNMKNKLYLDHMHVAIAINKSIDOELFDLYDLISDTIKGN	60
Db	61	YDKVKTLLNEDLNAKKKYKDEYVDVYDYSNYYNCAFESSK-DNW-GKLYGG-KTCMYGGITK	117
	61	: :	
Qy	61	YDNKRYEKKNDLADKTYKDYVDFGANYIYQCFISKTKINDINSHEIDKRTKMTGGYTE	120
Db	118	HEGNHFDGNLQNVLYRVEYENKRRNTISEFVOTDKSVTAOELDIKARNFLLKNKLYEFN	177
	118	: : : : : : : :	
Qy	121	HNGQLODK-Y-RSTIVRYEEDGKNLISDEDVQTNKKKVTYAOELDLTRHLYLVKNKKLYEFN	178
Db	178	SSPEYTGIRKLENNGNFEWDDMPAPEDKEDQSKYLLMYNDKNTQSKRKYIEVHLITK	237
	178	:	
Qy	179	NSPEITGIKFIENE-NSFWDDMPAPEDKEDQSKYLLMYNDKNTQSKRKYIEVHLITK	237
Db	238	N 238	

RESULT	ID	PRELIMINARY;	PRT;	239 AA.
	006535			
AC	006535;			
DT	01-NOV-1996 (Tremblrel. 01, Created)			
DT	01-NOV-1996 (Tremblrel. 01, last sequence update)			
DT	01-NOV-1999 (Tremblrel. 12, last annotation update)			
DE	ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/staphylococcus group; Staphylococcus.			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-FRI 909;			
RX	MEDLINE; 94011313.			
RA	MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;			
RT	"Characterization of novel type C staphylococcal enterotoxins;			
RL	biological and evolutionary implications.";			
FT	Infect. Immun. 61:4254-4262(1993)			
CC	-I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION			
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.			
CC	-I- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES			
CC	PYROGENIC EXOTOXINS ARE ALL RELATED.			
DR	EMBL; L13377; AAA26621.1; "-			
DR	HSSP; P2313; JTKC.			
DR	PFAM; PF01123; Staph_Stp_toxin; 1.			
KM	Enterotoxin; toxin; Superantigen.			
FT	NON_TER			
RD	SEQUENCE 239 AA; 27648 MW; 1DC80C35 CRC32;			

Query Match	64.9%;	Score 1145;	DB 2;	Length 239;
Best Local Similarity	64.3%;	Pred. No. 9.52e-189;		
Matches 155; Conservative	44;	Mismatches 36;	Indels 6;	Gaps 6;

Db	1	ESQDPMDDDLHKSSEFGTGMGNKKLYLTDHHYVSATKYKSVDRKLADHLIYNINHKTLNN	60
Qy	1	ESQDPKPKDELHKSSEKFTGLMKNKVALYLDHNNHVSALINKS:IDQELLYPDLIYSIDQTLGN	60
Db	61	YDKVTELLNEDLAKNKYKDEVDVYGSNNYVNCYFSSK-DNV-KGVTSG-KTCMYGIGTK	117
Qy	61	YDNVAVEEKNNDLADKYKDKYVDVFGANYYQCYFSKKTNDINSHEDRKRTCMYGGVTE	120
Db	118	HEGHNEDGNLQNVLLRYENKKNRTISFEVQTDKSVTAQELDIKARNELINKKNLYEFN	177
Qy	121	HNGNQLDK-Y-RSIVRFYFEDGKNLLSPDVOGNTKKKVTQAQELDYLTRHYLVKNNKLYEFN	178
Db	178	SSPYTGIKIKTIESGNTFFWDDMAPDPDKDQSKYLMYIKDNKMDVSKKIEVHLTTK	237
Qy	179	NSPYTGKIKTIE-NENSFWDMPAPDPKEDQSKYLMYINDKMDVSKDKVIEVYLTTK	237
Db	238	N 238	
Qy	238	K 238	
RESULT	7	PRELIMINARY:	PRT: 239 AA.
ID	005157		
AC	005157		
DT	01-JUL-1997	(TREMBLrel. 04, Created)	
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)	
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)	
DE	TYPE C ENTEROTOXIN (FRAGMENT).		
OS	Staphylococcus intermedius		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;		
OC	Bacillus/Staphylococcus group; Staphylococcus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-95-011195.		
RA	EDWARDS V.M., DERINGER J.R., CALLANTINE S.D., DEGBALD C.F.,		
RA	BEUGER P.H., KAPUR V., STAUFACHER C.V., BOHACH G.A.;		
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBV databases.		

OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS 1842;
RA MEDLINE; 94222556.
R REDA K.B., KAPUR V., MOLLICK J.A., LAMPHEAR J.G., MUSSER J.M.,
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS 1842;
R MEDLINE; 96178602.
RA REDA K.B., KAPUR V., GOELA D., LAMPHEAR J.G., MUSSER J.M., R.R.;
RT "Phylogenetic distribution of streptococcal superantigen Ssa allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes.";
RL Infect. Immun. 64:1161-1165(1996).
R EMBL; U48793; AAB02149.1; -.
DR HSSP; P34071; 1SE2.
DR PFAM; PF01123; Strep_toxin; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
SQ SEQUENCE 260 AA; 29836 MM; 3069EA84 CRC32;

Query Match 61.3%; Score 1081; DB 2; Length 260;
Best Local Similarity 62.4%; Pred. No. 2,01e-16;
Matches 148; Conservative 38; Mismatches 44; Indels 7; Gaps 6;

DB 29 QDPDPKLNKSOFTGVGNLRCLYDNHFEVGTNVRSTGOLLOHLPIDKLNKD 88
OY 3 QDPDPKDELHSSKSKFTGLMNMKVLXDNNHSAINVSIDOLFYLIDLIYSTDTLGND 62
DB 89 SVKTEFNSKDLAKYKNDVDIFGSNYYNYCYSE-GN--SCKNA-K-KTCMYGVTEHH 143
OY 63 NVRFVFKKDLADKXKDYVFGANYYYQCYFSKKTNDINSHEDDKRTCTMGYGTENN 122
DB 144 RNOIGKFPNTIVKYEDNENILSFDTITNKQVVOELDCFKILYSRKMLYEPNSP 203
OY 123 GNQLD-KYRSTIVRVEEDGKNLSFDVOTNKKRYAQLDYLTRYLYVKNKKLYEFNNSP 181
DB 204 YETGYIKFESSGDSFWYDMPAPGAIPOSKYLMJYNDNKTVSSAALIEVHLTK 260
OY 162 YETGYIKFLENE-NSFWYDMPAPGDKFDQSKYLMYNDNKKWVDSKVIEVLYTK 237
RESULT 11
ID 085382 PRELIMINARY; PRT; 258 AA.
AC 085382;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 12, Last annotation update)
DE EXTRACELLULAR ENTEROTOXIN TYPE G PRECURSOR.
GN SEG.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRI572;
R MEDLINE; 98298056.
RA MUNSON S.H., TREMAINE M.T., BETLEY M.J., WELCH R.A.;
RT "Identification and characterization of staphylococcal enterotoxin
RT types G and I from Staphylococcus aureus.";
RL Infect. Immun. 66:3337-3348(1998).
R EMBL; AF064773; AAC26660.1; -.
DR HSSP; P01552; 1SE3.
DR PFAM; PF01123; Strep_toxin; 1.
DR SIGNAL.
FT CHAIN 1 25 POTENTIAL.
FT SIGNAL 26 258 ENTEROTOXIN TYPE G.
SQ SEQUENCE 258 AA; 29940 MM; 14BDEBE CRC32;

Query Match 40.7%; Score 718; DB 2; Length 258;
Best Local Similarity 45.6%; Pred. No. 3.06e-107;
Matches 110; Conservative 54; Mismatches 65; Indels 12; Gaps 8;
DB 24 NAQDPKIDELKLVSDYKNNKGTMGNMVLYSPPEVGRGVNSKROFLSHDLIPI-EYK 82
OY 1 ESQDPKDELHSSKSKFT---GLMNMKVLXDNNHSAINVSIDOLFYLIDLIYSTDK 57
DB 83 --SYNEVKTELENTELANNKYDKKVDIFGVYFYCIIPKSEPDIN-QNFGG--CCMYG 137
OY 58 LGNYDNVRYEVEFKNKDLADKXKDYVFGANYYYQCYFSKKTNDINSHEDDKRTCTMG 117
DB 138 LT-FNSSENERDKLITVOYTIIDNROSIGFTITNKNMVTIOELDYKARHMLTKKKLYE 196
OY 118 VTEHNGNOLDKXRSITVRFEEDGKNLSFDVOTNKKRYAQLDYLTRYLYVKNKKLYE 177
DB 197 DGSAPESGYIKFTEKNNTSFWFDLPFKKELVFPVYKFLNIYDGNKVVDSKIKMEVFLN 256
OY 178 NNSPYETGYIKFTEKENN-SFWYDMPAPG-DKFDQSKYLMYNDNKKWVDSKVIEVLYT 235
DB 257 T 257
OY 236 T 236

RESULT 12
ID 092NF2 PRELIMINARY; PRT; 258 AA.
AC 092NF2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE ENTEROTOXIN TYPE GV.
GN SEG2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RA ABE J.;
RT "Staphylococcal Enterotoxin.";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB016487; BAA36693.1; -.
DR HSSP; P01552; 1SE3.
SQ SEQUENCE 258 AA; 29839 MM; 34E42F0F CRC32;
Query Match 40.3%; Score 710; DB 2; Length 258;
Best Local Similarity 45.2%; Pred. No. 9.79e-106;
Matches 109; Conservative 55; Mismatches 65; Indels 12; Gaps 9;
DB 24 NAQDPKIDELKLVSDYKNNKGTMGNMVLYSPPEVGRGVNSKROFLSHDLIPI-EYK 82
OY 1 ESQDPKDELHSSKSKFT---GLMNMKVLXDNNHSAINVSIDOLFYLIDLIYSTDK 57
DB 83 --SYNEVKTELENTELANNKYDKKVDIFGVYFYCIIPKSEPDIN-QNFGG--CCMYG 137
OY 58 LGNYDNVRYEVEFKNKDLADKXKDYVFGANYYYQCYFSKKTNDINSHEDDKRTCTMG 117
DB 138 LT-FNSSENERDKLITVOYTIIDNROSIGFTITNKNMVTIOELDYKARHMLTKKKLYE 196
OY 118 VTEHNGNOLDKXRSITVRFEEDGKNLSFDVOTNKKRYAQLDYLTRYLYVKNKKLYE 177
DB 197 DGSAPESGYIKFTEKNNTSFWFDLPFKKELVFPVYKFLNIYDGNKVVDSKIKMEVFLN 256
OY 178 NNSPYETGYIKFTEKENN-SFWYDMPAPG-DKFDQSKYLMYNDNKKWVDSKVIEVLYT 235
DB 257 T 257
OY 236 T 236
RESULT 13
ID 054696 PRELIMINARY; PRT; 236 AA.
AC 054696;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61573; CAA43771.1; -.
DR HSSP; P34071; 1SE2.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_Strep_toxin; 1.
KW Signal.
FT NON_TER 1 22 POTENTIAL.
FT SIGNAL 23 >236 TYPE A EXOTOXIN.
FT CHAIN 23 236
FT NON_TER 236
SQ SEQUENCE 236 AA; 27575 MW; A799A5F3 CRC32;

Query Match 39.9%; Score 704; DB 2; Length 236;
Best Local Similarity 46.5%; Pred. No. 1,32e-104;
Matches 107; Conservative 53; Mismatches 54; Indels 16; Gaps 8;

Db 22 AQQDPNSQLHRSSLVNKL-QNIYFLYEGDPVYHENKSVQQLSHDLIVNSG--L-NY 77
QY 2 SQDPKPELHKSSKFTGLMNMKVLTDNHNVAINVKSIDQFLYFDLITSIKDTKLGNY 61
DB 78 DKLTELKNDQEMATLFDKNVDIVGEYHYHLYC-----E-NA-----RSACIYGVYTNH 128
QY 62 DNVAVEFKNKDLADKYDVFGANYIYCYCSKKTNDINSHTDCKRKCMTGVTEN 121
DB 129 EGNHLEIPKNTLVKVSIDGQSLSFDIETSKKMTVAQELDYKVKHLLTDNKQLYTNGPSK 188
QY 122 NGNOLDKYRSTIVYFDEGKMLLSFDVQTNKKVTAQELDYLTRHLYLVKNNKLYEFNNSP 181
DB 189 YETGYIKFIKSKDETFWDFPEEP-E-FNQYKLYMIYKNDNTLSNTSQI 236
QY 182 YETGYIKFIENEN-SFWYDMMPAPGDFDQSKYLMATYNDNMKAVDSKDVKI 230

RESULT 14
ID P97163 PRELIMINARY; PRT; 236 AA.
AC P97163; P97164;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156; AND MGAS500;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61556; CAA43754.1; -.
DR EMBL; X61557; CAA43755.1; -.
DR EMBL; X61560; CAA43758.1; -.

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DR EMBL; X61555; CAA43753.1; -.
DR EMBL; X61558; CAA43756.1; -.
DR EMBL; X61559; CAA43757.1; -.
DR EMBL; X61554; CAA43752.1; -.
DR HSSP; P01552; 1SE3.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_Strep_toxin; 1.
KW Signal.
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FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
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Query Match 39.5%; Score 696; DB 2; Length 236;
Best Local Similarity 48.7%; Pred. No. 4,20e-103;
Matches 112; Conservative 43; Mismatches 59; Indels 16; Gaps 9;

Db 22 AQQDPDSQLHRSSLVNKL-QNIYFLYEGDPVYHENKSVQQLSHDLIVNSG---NY 77
QY 2 SQDPKPELHKSSKFTGLMNMKVLTDNHNVAINVKSIDQFLYFDLITSIKDTKLGNY 61
DB 78 DKLTELKNDQEMATLFDKNVDIVGEYHYHLYC-----E-NA-E-----RSACIYGVYTNH 128
QY 62 DNVAVEFKNKDLADKYDVFGANYIYCYCSKKTNDINSHTDCKRKCMTGVTEN 121
DB 129 EGNHLEIPKNTLVKVSIDGQSLSFDIETSKKMTVAQELDYKVKHLLTDNKQLYTNGPSK 188
QY 122 NGNOLDKYRSTIVYFDEGKMLLSFDVQTNKKVTAQELDYLTRHLYLVKNNKLYEFNNSP 181
DB 189 YETGYIKFIKSKDETFWDFPEEP-E-FNQYKLYMIYKNDNTLSNTSQI 236
QY 182 YETGYIKFI-ENEN-SFWYDMMPAPGDFDQSKYLMATYNDNMKAVDSKDVKI 230

RESULT 15
ID 054779 PRELIMINARY; PRT; 236 AA.
AC 054779; 054613; 054736; 054740; 054741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RX MEDLINE; 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61569; CAA43767.1; -.
DR EMBL; X61572; CAA43770.1; -.
DR EMBL; X61568; CAA43766.1; -.
DR EMBL; X61570; CAA43768.1; -.
DR EMBL; X61571; CAA43769.1; -.
DR HSSP; P01552; 1SE3.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_Strep_toxin; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA; 27468 MW; E902ED6D CRC32;

Query Match 39.4%; Score 694; DB 2; Length 236;

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• Sat Apr 22 12:33:42 2000

Best Local Similarity 48.38; Pred. No. 9,98e-103;
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Search completed: Thu Apr 20 15:13:37 2000
Job time : 223 secs.

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